

Figure 1

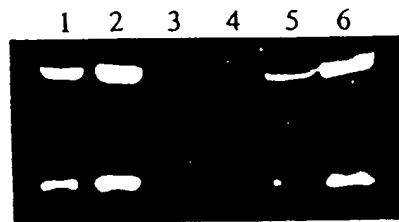


Figure 2

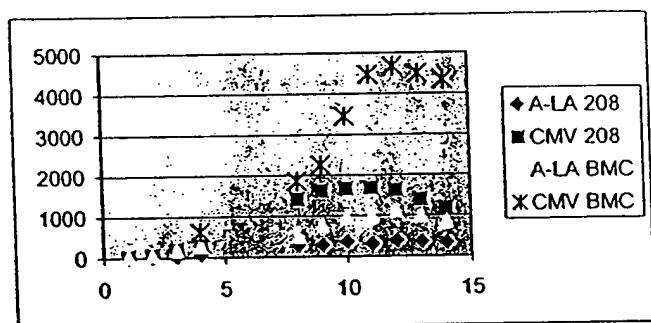
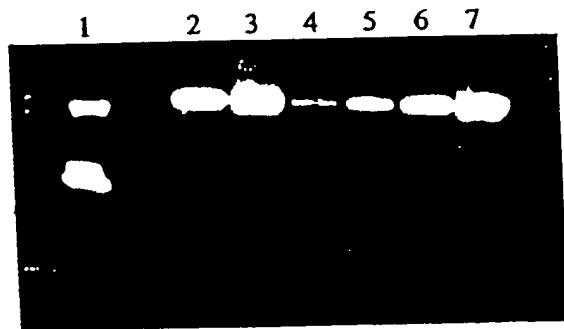


Figure 3



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Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

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1      GATCAGTCCTGGGTGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51     AACTTTGGCCACCTGATGCGAAGAAGTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
101    ATACTGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151    GAGTTGGATGGAATCACCACCGATGGACATGAGTTGAGCAAGCTTCC
201    AGGAGTTGGTAATGGGCAGGGAAAGCCTGGCGTGTGCACTCCATGGGGTT
251    GCAAAGAGTTGGCAACTGAGTGACTGAAGTCAACTGATAGTGTAAATC
301    CATGGTACAGAATATAGGATAAAAAGAGGAAGAGTTGCCCCGATTCG
351    AAGAGTTGAGGATATAAAAGTTAGAATACCTTAGTTGAGCTTAA
401    ATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451    AGAGACTGATGAGAGAATGAGCCCTGGCATACAGAAGCTAACAGCT
501    ATTGGTTATAGCTGTTAACCAATATATAACCAATATATTGGTTATATA
551    GCATGAAGCTTGATGCCAGCAATTGAGGAACCCATTAGAAGCTAGTATC
601    CTAACACTCATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAAGAAT
651    CTGTTTTATAGGCTCTAGGTGTATATTGAGGGCTTCCCTGGCTCA
701    GATGGTAAAGTGTCTGCCATGTGGGTGATCTGGGTTGATCCCCTGG
751    CTTGGGAAGATCCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801    ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAAGCTACAGTCCATGGG
851    ATTGCAAAGAGGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
900    ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951    ATTGCAGAAAGATTCTTACCATGTCAGGCCACAGGGAAAGCCAAGAATA
1001   CTGGAGTGGGTAGCCTATCCTCTCCAGGGGATCTTCCCACATCCCAGGAA
1051   TTGAACTGGAGTCTCTGCATTTCAGGTGGATTCTCACCAGCTGAACTA
1101   CCAGGTGGATACTCTCAATATTAAAGTGTAAAGTCCAGTTTTCCCA
1151   CCTTCCCCAAAAGGGTGGTCACTTTTTAACCTTCTGTGGCCTACT
1201   CTGAGGCTGCTACAAGCTTATATATTATGAACACATTTATTGCAAGTT
1251   GTTAGTTTAGATTACAATGTGGTATCTGGCTATTAGTGGTATTGGTG
1301   GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351   ATACACACTTTCAAGTCTCCATTGGTGAATAGAAAGTCTCTGGAT
1401   CTAAGTTATATGTGATTCTCAGTCTGTGGTCATATTCTATTCTACTCC
1451   TGACCACTCAACAAGGAACAGATATCAAGGGACACTTGTGGTTCA
1501   TGCGGGTTGAGTGGGGCATGACATATGTTCTGGGCTTGTACATGGC
1551   TGAGATTGGTGGACAAGTGCCTGACTGATCCTGGGACTGTGGCATGTGA
1601   TGACATACACCCCTCTCCACATTGTCATGTCCTAGGGGGAGGGGG
1651   AAGCTCGGTATAGAACCTTATTGTATTCTGATTGCCACTTCTTAT
1701   ATTGCCCCCATGCCCTTCTTGTCTCAAGTAACCAAGAGACAGTGCCTC
1751   CCAGAACCAACCCCTACAAGAAACAAAGGGCTAAACAAAGCCAATGGGAA
1801   GCAGGATCATGGTTGAACTCTTCTGGCCAGAGAACAACTGCTATG
1851   GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901   AGCTGGCAGGCTCAGCGTTCTGTCTGGCATGACAGCTCTCTCATT
1951   CTCTTCTAGATGTAGGGCTTGGTACCAAGAGCCCTGAGGGTTCTGCAT
2001   GAATATAAAATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTGGGG
2051   GCGCGAATTGAGCTCGGTACCCGGGATCTCGAGGGGGCCCGGTAC
2101   C

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1 - 1525 Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)

1526 - 2056 Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)

2057 - 2101 Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

1 GATTACTTACTGGCAGGTGCTGGGGCTTCCGAGACAATCGCGAACATCT
51 ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGACGCG
101 GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151 GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201 AGGGTGAGATATCGGCCGGGACGCCGGTGGTAATTACAAGCG

1 - 119 Mutated PPE
120 -126 Linker
127 - 245 Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

1 GGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCGAAGCCG
51 CTTCCAATAAGGCCGGTGTGCGTTGTCTATATGTTATTTCCACCATAT
101 TGCCTCTTTGGCAATGTGAGGGCCGGAAACCTGGCCCTGTCTTCTG
151 ACGAGCATTCCCTAGGGCTCTTCCCCCTCGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTTCTTGAAGACAAA
251 CAACGTCTGTAGCGACCCCTTGCAAGCAGCGGAACCCCCCCTGGCGAC
301 AGGTGCCTCTGCCGCCAAAGCCACGTGTATAAGATAACACCTGCAAAGGC
351 GGCACAAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTC
401 AATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCAGAAAG
451 GTACCCCATTGTATGGGATCTGATCTGGGCTCGGTGCACATGCTTTAC
501 ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCGAACACGGGG
551 ACGTGGTTCTCTTGAAACACGATGATAATATGGCCTCCTTGTCTC
601 TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651 GATATCTAGATCTCGAGCTCGCAGAAAGCTT

1 - 583 IRES
584 - 640 Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680 Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

1 CCGATCCGCCATTAGCCATTATTATTGTTATAGCATAATCAA
 51 TATTGGCTATTGGCATTGCATACGTTGATCCATATCATAATATGTACA
 101 TTTATATTGGCTCATGTCACATTACGCCATTGGCTATAGTCAGCCATA
 151 ACTAGTTATAATAGTAATCAATTACGGGCTATAGTCAGCCATA
 201 TATGGAGTCCCGCTTACATAACTACGGTAAATGGCCCGCTGGCTGAC
 251 CGCCCAACGACCCCCGCCCCATTGACGTCATAATGACGTATGTTCCATA
 301 GAACTGCAATAGGACTTCCATTGACGTCATAATGGGTGGAGTATTTACG
 351 GAAACTGCCCACGGCAAGTACATCAAGTGTATCATATGCCAGTACGC
 401 CCCCTATTGACGTCATGACGGTAAATGGCCCGCTGGCATTATGCCAG
 451 TACATGACCTTATGGGACTTCCTACTTGGCAGTACATCTACGTATTAGT
 501 CATCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATGGCGTG
 551 GATAGCGGTTGACTCACGGGATTTCAAGTCTCCACCCATTGACGTC
 601 AATGGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAAATGTCG
 651 TAACAACCTCCGCCATTGACGCAATGGGCGGTAGGCATGTACGGTGG
 701 AGGTCTATATAAGCAGAGCTGTTAGTGAACCGTCAGATGCCCTGGAGA
 751 CGCCATCCACCGCTGTTGACCTCCATAGAAGACACCGGGACCGATCCAG
 801 CCTCCGGGCCCAAGCTCTCGACGGATCCCCGGAAATTCAAGGACCTCA
 851 CCATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGT
 901 GTCCACTCCGAGGTCAACTGGTGGAGAGCGGTGGAGGTGTGCAACC
 951 TGGCCGGTCCCTGCGCTGTCCCTGCTCCGCATCTGGCTTCGATTTCACCA
 1001 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
 1051 ATTGGAGAAATTCTACAGATAGCAGTACGATTAACTATGCCGTCTCT
 1101 AAAGGATAGATTACAATATCGCGAGAACAGCAAGAACACATTGTTCC
 1151 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGCTATTGGTGCA
 1201 AGCCTTACTTCGGCTTCCCTGGTTGCTTATTGGGGCCAAGGGACCC
 1251 GGTCAACCGTCTCCTCAGCCTCCACCAAGGGCCATGGCTTCCGGCTGG
 1301 CACCCCTCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCC
 1351 GTCAGGACTACTCCCGAACCGGTGACCGTGTGGAAACTCAGGCC
 1401 CCTGACAGCGCGTGACACCTTCCGGCTGACCTTCAGCTCAGGCC
 1451 TCTACTCCCTCAGCGTGGTGACCGTGGCTCCAGCAGCTGGGACCC
 1501 CAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACACCAAGGTGG
 1551 CAAGAGAGTTGAGCCAAATCTTGTGACAAGTACACATGCCACCGT
 1601 GCCCAGCACCTGAACCTGGGGGACCGTCAGTCTTCCCTCTCCCCCA
 1651 AAACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGT
 1701 GGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACG
 1751 TGACCGCGTGGAGGTGATAATGCCAAGAACAGCCGGGGAGGAGCAG
 1801 TACAACAGCACCGTACCGTGTGGTACCGTCTCACCGTCTGCACCAAGGA
 1851 CTGGCTGAATGGCAAGGAGTACAAGTGCAGGTCTCAACAAAGCCCTCC
 1901 CAGCCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCGAGAA
 1951 CCACAGGTGTACACCCCTGCCCATCCGGAGGAGATGACCAAGAACCA
 2001 GGTCAAGCTGACCTGGTCAAAGGCTTCTATCCCAGCGACATGCC
 2051 TGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCC
 2101 CCCGTGCTGGACTCCGACGGCTCTTCTCTATAGCAAGCTCACCGT
 2151 GGACAAGAGCAGGTGGCAGCAGGGGAAACGTCTTCATGCTCCGTGATGC
 2201 ACGAGGCTCTGCACAACCAACTACACGCAGAAGAGCCTCTCC
 2251 GGGAAATGAAAGCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTAA
 2301 CTGGCCGAAGCCGTTGGAATAAGGCCGGTGTGCGTTGTATATGTTA
 2351 TTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCCGGAAACCTGG
 2401 CCCGTCTCTTGTGACGAGCATTCTAGGGCTTCTCCCTCTGCCAAAG
 2451 GAATGCAAGGTGTGAATGTCGTGAAGGAAGCAGTCCCTGTCTCC
 2501 TCTTGAAGAACAAACCGTCTGTAGCGACCCCTTGCAGGCAAGC
 2551 CCCACCTGGCGACAGGTGCCTCTGCCCAAAAGCCACGTGATAAGATA
 2601 CACCTGCAAAGCGGACAACCCCAAGTGCACCTGTGAGTTGGATAGTT
 2651 GTGGAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAA
 2701 GGATGCCAGAAGTACCCATTGATGGGATCTGATCTGGGCCCTCGGT
 2751 GCACATGCTTACATGTGTTAGTCGAGGTAAAAAAACGTCTAGGCCCC
 2801 CCGAACCAACGGGACGTGGTTCTTGTGAAACACGATGATAATATGG

Figure 7b

2851 CCTCCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAG
2901 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
2951 TGACAGAGTGACCATCACCTGTAAGGGCCAGTCAGGATGTGGGTACTTCTG
3001 TAGCCTGGTACCGAGCAGAAGCCAGGTAAAGGCTCCAAAGCTGCTGATCTAC
3051 TGGACATCCACCCGGCACACTGGTGCCAAGCAGATTCAAGCGTAGCGG
3101 TAGCGGTACCGACTTCACCTCACCATCAGCAGCCTCAGGCCAGAGGACA
3151 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTGTTCGGCCAA
3201 GGGACCAAGGTGAAATCAAACGAACGTGGCTGCACCATCTGTCTTCAT
3251 CTTCCGCCATCTGATGAGCAGTTGAAATCTGGAACGTGCCTCTGTGT
3301 GCCTGCTGAATACTCTATCCAGAGAGGCCAAGTACAGTGGAAAGGTG
3351 GATAACGCCCTCCAATCGGTAACTCCAGGAGAGTGTACAGAGCAGGA
3401 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAG
3451 CAGACTACGAGAAAACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC
3501 CTGAGCTGCCGTCAAAGAGCTTCAACAGGGAGAGTGTAGAGATC
3551 TAGGCCTCTAGGTCGACATCGATAAAAATAAAAGATTTATTAGTCCTCC
3601 AGAAAAAGGGGGAAATGAAAGACCCCACCTGTAGGTTGGCAAGCTAGCT
3651 TAAGTAACGCCATTTCGAAAGGCATGAAAAATACATAACTGAGAATAGA
3701 GAAGTTCAGATCAAGGTAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751 ACAGGATATCTGTTGAGCAGTTCTGCCCCGGCTCAGGGCCAAGAACAA
3801 GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTTGAGCAGTT
3851 CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
3901 CTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGGAC
3951 CTGAAATGACCCGTGCCCCATTGAACTAACCAATCAGTTGCTTCTCG
4001 CTTCTGTTCGCGCGTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAAC
4051 CCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGCCGGTACCC
4101 GTGTATCCAATAAAACCTCTTGCAAGTTGCATCCGACTTGTGGTCTCGCTG
4151 TTCTGGGAGGGTCTCTTGAGTGATTGACTACCCGTAGCGGGGGTC
4201 TTTCATT

1 - 812 CMV promoter/enhancer
853-855 MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259 MN14 antibody heavy chain gene start codon
2271 - 2846 EMCV IRES
2847 - 2849 Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906 First codon mature MN14 antibody light chain gene
3543 - 3544 MN14 antibody light chain gene stop codon
3614 - 4207 MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

1 GGATCCGGCATTAGCCATTATTCAATTGGTTATATAGCATAATCAAT
 51 ATTGGCTATTGGCATTGCACTCGTGTATCCATATCATAATATGTACAT
 101 TTATATTGGCTCATGTCAACATTACCGCCATGGACATTGATTATTGA
 151 CTAGTTATTAAATAGTAATCAATTACGGGGCATTTAGTCATAGCCCATAT
 201 ATGGAGTTCCCGTACATAACTTACCGTAAATGGCCGCTGGCTGAC
 251 GCCCAACGACCCCCGCCATTGACGTCAATTACGGGTGGAGTATTTACGG
 301 TAACGCCAATAGGGACTTCCATTGACGTCAATTACGGTATGTTCCCATAG
 351 TAAACTGCCCATTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
 401 CCTATTGACGTCAATTGACGGTAAATGGCCGCTGGCATTATGCCAGT
 451 ACATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAGTC
 501 ATCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATTGGCGTGG
 551 ATAGCGGTTTACTCACGGGATTCCAAGTCTCACCCATTGACGTCA
 601 ATGGGAGTTTGTGACCAAAATCAACGGGACTTCCAAGTGTACGGTGGGA
 651 AACAACTCCCGCCATTGACGCAAATGGCGTAGGCATGTACGGTGGGA
 701 GGTCTATATAAGCAGAGCTCGTTAGTGAACCGTCAGATCGCCTGGAGAC
 751 GCCATCCACGCTGTTTGACCTCCATAGAAGACACCGGACCGATCCAGC
 801 CTCCGCGGCCAAGCTCTCGACGGATCCCCGGAATTAGGACCTCAC
 851 CATGGGATGGAGCTGTATCATCCTCTTGGTAGCAACAGCTACAGGTG
 901 TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGCTGAAGTCAAGAACCT
 951 GGGTCATCAGTGAAGGTCTCTGCAAGGCTTCTGGTACACCTTTACTAG
 1001 CTACTGGCTGCACTGGGTCAAGGCACCTGGACAGGGCTGGAAATGGA
 1051 TTGGATACATACTCTAGGAATGATTACTGAGTACAATCAGAACTTC
 1101 AAGGACAAGGCCACAATACTGAGGCAATCCAAATACAGCCTACAT
 1151 GGAGCTGAGCAGCTGAGGTCTGAGGACACGGCATTTTATTTGTGCAA
 1201 GAAGGGATATTACTACGTTCTACTGGGGCAAGGCACACGGTACCGTC
 1251 TCCTCAGCCTCCACCAAGGGCCATGGTCTCCCCCTGGCACCCCTC
 1301 CAAGAGCACCTCTGGGGCACAGGCCCTGGCTGCCTGGTAAGGACT
 1351 ACTTCCCAGCGTGAAGGTGCTGGAACTCAGGCGCCCTGACCCAGC
 1401 GGCCTGCACACCTTCCCGTGTCTACAGTCCTCAGGACTCTACTCC
 1451 CAGCAGCTGGTACCGTCCAGCAGCTGGCACCCAGACCTACA
 1501 TCTGCAACGTGAATCACAAGCCCAGAACACCAAGGTGGACAGAGATT
 1551 GAGCCAAATTTGTGACAAAATCACACATGCCAACCGTCCCCAGCACC
 1601 TGAACCTCTGGGGGACCGTCAGTCCTCTTCCCCAAAACCCAAGG
 1651 ACACCCCTCATGATCTCCCGACCCCTGAGGTCAATGCGTGGTGGAC
 1701 GTGAGGCCAGAAGACCTGAGGTCAAGTCAACTGGTACGTGGACGGGT
 1751 GGAGGTGCAATAATGCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCA
 1801 CGTACCGTGTGGTCAAGCTCCTCAGCTCTGACCCAGGACTGGCTGAAT
 1851 GGCAGGGAGTACAAGTGCAGGTCTTCAAAACAGCCCTCCAGCCCCAT
 1901 CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGT
 1951 ACACCCCTGCCCTATCCGGGAGGAGATGACCAAGAACCCAGGTCAAGCTG
 2001 ACCTGCCCTGGTCAAAGGTTCTATCCCAGCGACATGCCGTGGAGTGGGA
 2051 GAGCAATGGCAGCCGAGAACAAACTACAAGACCAAGCCTCCGTGTGG
 2101 ACTCCGACGGCTCTTCTCTATAGCAAGCTACCGTGGACAAGAGC
 2151 AGGTGGCAGCAGGGGAAACGTCTTCTCATGCTCGTGTGACAGGGCTCT
 2201 GCACAACCACTACAGCAGAACAGGGCTCTCCCTGTCTCCCCGGAAATGAA
 2251 AGCCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGCCGAAG
 2301 CCGCTGGATAAGGCCGTGCGTTGTCTATGTTATTTCCACCA
 2351 TATTGCCGTCTTGGCAATGTGAGGGCCGAAACCTGGCCCTGTCTTC
 2401 TTGACGAGCATTCTAGGGGTCTTCCCTCTGCCAAAGGAATGCAAGG
 2451 TCTGTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAGCTCTGAAGAC
 2501 AAACAACTCTGTAGCCACCCCTTGCAGGCAGGGAACCCCCCACCTGGC
 2551 GACAGGTGCCCTCTGCCGCCCCAACGGCACGTGATAAGATACACCTGCC
 2601 GGCAGCACAACCCAGTGCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
 2651 TCAAATGGCCTCTCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAG
 2701 AAGGTACCCATTGTATGGGATCTGATCTGGGGCTCGGTGCACATGCTT
 2751 TACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGAACACAG
 2801 GGGACGTGGTTTCTTGGGATCTGATCTGGGGCTCGGTGCACATGCTT

Figure 8b

2851 CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901 AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGGAGATAGGGTC
2951 ACTATGAGCTGTAAGTCCAGTCAAAGTGTATACAGTCACAA
3001 GAACTACTGGGCTGGTACCGAGAAACCAGGGAAAGCACCCTAAACTGC
3051 TGATCTACTGGCATTCCACTAGGGAACTCTGGTGTCCCTCGCGATTCT
3101 GGCAGCGGATCTGGGACAGATTTACTTCACCACATCAGCTCTTCAACC
3151 AGAACAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
3201 TCGGTGGAGGGACCAAGGTGAGATCAAACGAACACTGTGGCTGCACCATCT
3251 GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACACTGCCTC
3301 TGTTGTGTGCTGTAACTTCTATCCCAGAGAGGGCAAAGTACAGT
3351 GGAAGGTGGATAACGCCCTCAATCGGTAACTCCAGGAGAGTGTCA
3401 GAGCAGGACAGCAAGGACAGCACCTACGCCTCAGCAGCACCTGACGCT
3451 GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
3501 ATCAGGGCCTGAGCTGCCGTACAAGAGCTTCAACAGGGAGAGTGT
3551 TAGAGATCTAGGCCCTCTAGGTCGACATCGATAAAAATAAAAGATTTATT
3601 TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTGGCA
3651 AGCTAGCTTAAGTAACGCCATTGCAAGGCATGGAAAAATACATAACTG
3701 AGAATAGAGAAGTTCAGATCAAGGTCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751 TGGGCCAAACAGGATATCTGGTAAGCAGTTCTGCCCGGCTCAGGGC
3801 CAAGAACAGATGGAACAGCTGAATATGGCCAACAGGATATCTGTGGTA
3851 AGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCC
3901 GTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCC
3951 CCAAGGACCTGAAATGACCCGTGCCCCATTGAACTAACCAATCAGTT
4001 GCTTCTCGCTTCTGTTCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051 CCCACAACCCCTCACTCGGGCGCCAGTCCTCCGATTGACTGACTCGCCC
4101 GGGTACCCGTGATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGG
4151 TCTCGCTTCTGGGAGGGTCTCCTCTGAGTGAATGACTACCCGTCA
4201 GTCTTCATT

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

Figure 9a
SEQ ID NO:6
MMTV MN14 Vector

1 CGAGCTTGGCAGAAATGGTGAACCTCCGAGAGTGTCTACACCTAGGGG
 51 AGAAGCAGCCAGGGTTGTTCCACCAAGGACGACCCGTCGCGACA
 101 AACGGATGAGCCCCTACAGACAAAGACATATTCTCTGCTGCAAACCTT
 151 GGATAGCTCTGCTTGCCTGGCTATTGGGGAAAGTTGCGGTCGTGC
 201 TCGCAGGGCTCTACCCCTGACTCTTCAATAAACTCTGTGCAAG
 251 ATTACAATCTAACAAATTCGGAGAACTCGACCTCCCTGAGGCAAGGA
 301 CCACAGCCAACCTCCCTTACAAGCCGATCGATTTGTCCTCAGAAAT
 351 AGAAAATAAGAATGCTTGCTAAAATTATTTTACCAATAAGACCAATC
 401 CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTTATCTTT
 451 AGTACTATTTTACTCAAATTCAAAGGTTAGAAATGGGAATAGAAAATAG
 501 AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
 551 CAGGCCTAGAAGTAAAAAGGGAAAAAAAGAGTGTGTCAGGAAATAGGA
 601 GACAGGTGGTGGCAACCCAGGGACTTATAGGGGACCTACATCTACAGACC
 651 AACAGATGCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
 701 GGTGGTTACAGTCATGGCTATAAGTGTATATAGATCCCTCCCTTT
 751 CGTAAAAGACTCGCCAGAGCTAGACCTCCTGGTGTATGTTGTCAGAAG
 801 AAAGAAAAGACGACATGAAACAACAGGTACATGATTATTTATCTAGGAA
 851 CAGGAATGCACTTTGGGAAAGATTTCACCAAGGAGGGGACAGTG
 901 GCTGGACTAATAGAACATTCTGCAAAAACCTATGGCATGAGTTATT
 951 TGATTAGCCTTGATGGCCAACCTTGCCTTCCAAAGGCTTAAGTAAGT
 1001 TTGGTTACACAACTGTTCTTAAACAAAGGATGTGAGACAAGTGGTTCC
 1051 TGACTTGGTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTCTATT
 1101 TTCCATGTTCTTGGAAATTATCCTATGTAATGCTTATGTA
 1151 AACCAAGATATAAAAGAGTGTGATTGGAGTAAACCTGCAACAGTCC
 1201 TAACATTCACCTTGTGTTGTGCTGTTGCCATCCCGTCTCCGCT
 1251 CGTCACTTATCCTTCACTTCCAGAGGGTCCCCCGCAGACCCGGCGAC
 1301 CCTCAGGTGCCGACTGCCAGCTGGCGCCCCAACAGGGACCCCTCGGA
 1351 TAAGTGACCCCTGCTTATTCTACTATTTGTTGCTGTTGTTGTTG
 1401 CTCTATCTGTGCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
 1451 GAACCAAGCTAGCCGGGTCAGCGATCCGATTACTACTGGCAGGTGC
 1501 TGGGGGCTCCGAGACAATCCGAACATCTACACCACACAACACCGCCTC
 1551 GACCAGGGTGAGATATCCGCCGGGACGCCGGCGTGGTAATTACAAGCGA
 1601 GATCCGATTACTACTGGCAGGTGCTGGGGCTCCGAGACAATCCGGA
 1651 CATCTACACCCACAAACGCCCTGCCAGCAGGGTGGAGATATCGGGGGGG
 1701 ACGGGGGGTGGTAAATTACAAGCGAGATCCCCGGGAAATTCAAGGACTCAC
 1751 CATGGGATGGAGCTGTATCATCCTCTTCTGGTAGCAACAGCTACAGGTG
 1801 TCCACTCCGGAGTCCAACCTGGTGGAGAGCGGTGGAGGTGTGCAACCT
 1851 GGCCTGGTCCCTGCCCTGCTCTGCCATCTGGCTTCGATTTCAACAC
 1901 ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGA
 1951 TTGGAGAAATTATCCAGATAGCAGTACGATTAACTATGCCGCTCTA
 2001 AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCT
 2051 GCAAATGGACAGCCTGAGACCCGAAGACACCCGGGTCTATTTGTC
 2101 GCCTTTACTCCGGCTCCCTGGTTGCTTATTGGGGCAAGGGACCCCG
 2151 GTCACCGCTCCCTCAGCCTCCACCAAGGGCCATGGCTTCCCTGGC
 2201 ACCCTCCTCCAAGAGCACCTCTGGGGCACAGCGCCCTGGCTGCC
 2251 TCAAGGACTACTTCCCGAACCGGTGACGGTGTGTTGAACTCAGGCC
 2301 CTGACCAGGGCGTGCACACCTCCGGCTGCTCTACAGTCCCTCAGGACT
 2351 CTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTGGCACC
 2401 AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
 2451 AAGAGAGTTGAGCCCAAATCTTGTGACAAAAACTCACACATGCC
 2501 CCCAGCACCTGAACTCTGGGGGACCGTCAGTCTCTTCCCTTCCCC
 2551 AACCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTACATGCGT
 2601 GTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGT
 2651 GGACGGCGTGGAGGTGCAATGCAAGACAAGCCGGGGAGGAGCAGT
 2701 ACAACAGCACGTACCGTGTGGTCAGCGTCCCTACCGTCTGCA
 2751 TGGCTGAATGGCAAGGAGTACAAGTGCAGGTTCTCAAACAAAGCC
 2801 AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAGGGCAGCCCCGAGAAC

Figure 9b

2851 CACAGGTGTACACCCCTGCCCCCATCCGGGAGGAGATGACCAAGAACCAAG
2901 GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATGCCGT
2951 GGAGTGGAGAGCAATGGCAGCCGAGAACAACTACAAGACCAAGCGCTC
3001 CCGTGCCTGGACTCGACGGCTCCTCTCTCTATAGCAAGCTCACCGTG
3051 GACAAGAGCAGGGTGGCAGCAGGGGAACGTCTTCTATGCTCCGTGATGCA
3101 CGAGGCTCTGCACAACCACACTACACGAGAAGAGCTCTCCCTGTCTCCCG
3151 GGAATGAAAGCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTAC
3201 TGGCCGAAGCCGCTTGGAAAATAGGGCGGTGTGCGTTGTCTATATGTTAT
3251 TTGCCCCATATTGCCGTCTTGGCAATGTGAGGGCCGGAAACCTGGC
3301 CCTGTCCTTCTGACGAGCATTCCTAGGGGTCTTCCCTCTGCCAAAGG
3351 AATGCAAGGCTGTTGAATGTCGTAGCGACCCCTTCAGGCAGCGGAACCC
3401 CTCAGACAAACACGCTGTAGCGACCCCTTCAGGCAGCGGAACCC
3451 CCACCTGGCAGGGTGCCTCTGGCCAAAGGCCACGTGTATAAGATAC
3501 ACCTGCAAAGCGGCACAACCCAGTGCACGTGTGAGTTGGATAGTTG
3551 TGAAAAGAGTCAAATGGCTCTCCTCAACCGTATTCAACAAGGGGCTGAAG
3601 GATGCCAGAGTACCCATTGATGGATCTGATCTGGGCTCGGTG
3651 CACATGTTTACATGTGTTAGTCGAGGTTAAAAAAACGTCAGGCCCC
3701 CGAACACGGGAGCTGGTTTCCCTTGAAAACACGATGATAATATGGC
3751 CCTCTTGTCTCTGCTCTGGTAGGCATCTTATCCATGCCACCCAGG
3801 CCGACATCCAGCTGACCCAGAGCCAAAGCAGCTGAGCGCCAGCGTGGGT
3851 GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTCTGT
3901 AGCCTGGTACCAAGCAGAACGCCAGGTAAGGCTCAAAGCTGCTGATCTACT
3951 GGACATCCACCCGGCACACTGGTGTGCAAGCAGATTCAAGCGGTAGCGGT
4001 AGCGTACCGACTTCACCTCACCATCAGCAGCTCCAGCCAGAGGACAT
4051 CGCCACCTACTACTGCCAGCAATATGCCCTATCGGTCTGTTGGGCAAG
4101 GGACCAAGGTTGAAATCAAACGAACTGTGGCTGACCCTGTCATC
4151 TTCCCGCCATCTGATGAGCAGTTGAATCTGGAACTGCCCTGTTGTG
4201 CCTGCTGAATAACTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGG
4251 ATAACGCCCTCAATGGGTAACTCCCAGGAGAGTGTACAGAGCAGGAC
4301 AGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
4351 AGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCC
4401 TGAGCTGGGGTCAACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATCC
4451 CCCGGCTGAGGAATTGATATCAAGCTTATCGATAATCAACCTCTGGA
4501 TTACAAAATTGTGAAAGATTGACTGGTATTCTTAACATATGTTGCTCCTT
4551 TTACGCTATGTGGATACGCTGCTTAAATGCCCTGTTATCATGCTATTGCT
4601 TCCCGTATGGCTTCTATTTCTCTCTTGATAAAATCTGGTTGCTGTC
4651 TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4701 CTGTTTGTGACGCAACCCACTGGTGGGCATTGCCACCCACTGT
4751 CAGCTCTTCCGGGACTTCGCTTCCCTCCCTATTGCCACGGCGGA
4801 ACTCATGCCGCCCTGCCCTGGCCCTGCTGGACAGGGGCTCGCTGTTGG
4851 GCACTGACAATTCCGTGGTGTGCTGGGGAAATCATGCTCTTCTTGG
4901 CTGCTGCCGTGTTGCCACCTGGATTCTGCCGGGAGCTCTGCTGTA
4951 CGTCCCTCGGCCCTCAATCCAGGGACCTTCCCTCCGCCCTGCTGC
5001 CGGCTCTGGCCCTCTCCGCTTCCGCCCTCAGACGAGTCGG
5051 ATCTCCCTTGGGCCGCTCCCCGCTGATGATAACCGTCAACATGATA
5101 AAATAAAAGATTTATTTAGTCTCCAGAAAAAGGGGGAAATGAAAGACCC
5151 CACCTGAGGTTGGCAAGCTAGCTTAAGGCAACGCCATTGCAAGGGCAT
5201 GAAAAAAATACATAACTGAGAAATAGAGAAGTTCAAGATCAAGGTAGGAACA
5251 GATGGAACAGCTGAAATGGCCAAACAGGATATCTGTTGAAAGCAGTT
5301 CTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5351 ACAGGATATCTGTTGAAAGCAGTCTGCCCTGCCGGCTCAGGGCCAAGAAC
5401 GATGGTCCCCAGATGCCGTCCAGGCCCTCAGCAGTTCTAGAGAACCATCA
5451 GATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCCTGTCGCTTATTG
5501 AACTAACCAATCAGTTCGCTTCTCGCTTCTGTCGCGCGCTTCTGCTCCC
5551 CGAGCTCAATAAAAGGCCACAACCCCTCACTGGGGGCCAGTCTCCC
5601 GATTGACTGAGTCGCCGGTACCGTGTATCCAATAACCCCTTGTGAG
5651 TTGCACTGGACTTGTGGTCTCGCTGTTCTGGAGGGTCTCCTCTGAGT
5701 GATTGACTACCCGTCAGCGGGGGTCTTCATT

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

Figure 10a
SEQ ID NO:7
Alpha-Lactalbumin MN14 Vector

1 AAAGACCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTGC
 51 AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTCAGATCAAGGTCA
 101 GGAACAAAGAAACAGCTGAATACCAAAACAGGATATCTGTGGAAGCGGTT
 151 CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
 201 AACAGGATATCTGTGGAAGCAGTCCCTGCCCGGCTCGGGGCAAGAA
 251 CAGATGGTCCCAGATGCGGTCCAGGCCCTCAGCAGTTCTAGTGAATCAT
 301 CAGATGTTCCAGGGTCCCCAAGGACCTGAAAATGACCTGTACCTTAT
 351 TTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTTCGCGCGCTCCGCT
 401 CTCCGAGCTCAATAAAAGAGCCCACAAACCCCTCACTCGGCGGCCAGTCT
 451 TCCGATAGACTGCGTCGCCGGTACCCGTTCCCAATAAGCCTCTTG
 501 CTGTTGCATCCGAATCGGTCTCGCTGTTCTGGGAGGGTCTCTCT
 551 GAGTGAATTGACTACCCACGACGGGGTCTTCATTGGGGGCTCGTCCGG
 601 GATTGGAGACCCCTGCCAGGGACCCGACCCACCAACCGGAGGTAAG
 651 CTGGCCAGCAACTTATCTGTCTGTCGATTGTCAGTGTCTATGTTG
 701 ATGTTATGCGCCTGCGTCTGACTAGTTAGCTAAGTAGCTCTGTATCTGG
 751 CGGACCCGTGGTGAACGAGTTCTGAACACCCGGCCAAACCCCTGG
 801 GAGACGTCCCAGGGACTTGGGGCGTTTGTTGTTGGCCGACCTGAGGAA
 851 GGGAGTCGATGGAATCCGACCCCGTCAAGGATATGTTGTTCTGGTAGGA
 901 GACGAGAACCTAAACAGTTCCCGCCTCCGCTGAATTTCGTTCTGGT
 951 TTGGAACCGAACGGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
 1001 TGTTGTCCTGCTGACTGTGTTCTGTTATGTCGAAATTAGGGC
 1051 CAGACTGTTACCACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGT
 1101 CGAGCGGATCGTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
 1151 TTACCTCTGCTCTGCAAGAATGGCAACCTTTAACGTCGGATGGCCGCGA
 1201 GACGGCACCTTAACCGAGACCTCATCACCCAGGTTAACGTCAGGTCTT
 1251 TTCACCTGGCCGATGGACACCCAGACCGAGGCTCCATACATGTCACCT
 1301 GGGAAAGCCTTGGCTTTGACCCCCCTCCCTGGGTCAGGCCCTTGTACAC
 1351 CCTAACGCTCCGCTCTTCCATCCGCCCCGTCCTCCCCCTTGA
 1401 ACCTCTCGTTCGACCCCGCTCGATCCTCCCTTATCCAGCCCTCACTC
 1451 CTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
 1501 GTTTCGATGATTGAACAAAGATGGATTGACCGCAGGTTCTCCGGCCGCTT
 1551 GGGTGGAGAGGCTATTGGCTATGACTGGGACAAACAGACAATCGGCTGC
 1601 TCTGATGCCCGCTGTTCCGGCTGTCAGCCAGGGGCCGGTTCTTTT
 1651 TGTCAGACCGACCTGTCGGTGCCTGAATGAACTGCAAGGACGAGGCAG
 1701 CGCGGCTATGTTGGCTGCCACGACGGCGTTCTGCGCAGCTGTGCTC
 1751 GACGTTGTCAGTGAAGCGGGAAAGGGACTGGCTGCTATTGGCGAAGTGCC
 1801 GGGGCAGGATCTCTGTCATCTCACCTGCTCTGCGAGAAAGTATCCA
 1851 TCATGGCTGATGCAATGCCGGCTGCATACGTTGATCCGGTACCTGC
 1901 CCATTGACCAACCGAAACATCGCATCGAGCGAGCACGTACTCGGAT
 1951 GGAAGCGGCTTGTGCGATCAGGATGATCTGGACGAAGGACATCAGGGGC
 2001 TCGCGCCAGCGAACCTGTCGGCTGCCAGGCTCAAGGCGCGATGCCGACGGC
 2051 GAGGATCTCGTGCAGGATGCCGATGCGCTGTTGCCGAAATATCATGGT
 2101 GGAAAATGGCGCTTTCTGGATTCTGACTGTGGCGGCTGGGTGTGG
 2151 CGGACCGCTATCAGGACATAGCGTGGCTACCCGTGATATTGCTGAAGAG
 2201 CTTGGCGGCGAATGGGTGACCGCTTCTCGTGTCTTACGGTATGCCGC
 2251 TCCCGATTGCGAGCGCATCGCCTCTATGCCCTTCTGACCGATTCTTCT
 2301 GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGC
 2351 CATCACGAGATTTCGATTCCACCGCCCTCTATGAAAGGTTGGGCTTC
 2401 GGAATGTTTCCGGGACGCCGGCTGGATGATCTCCAGCGCGGGGATCT
 2451 CATGCTGGAGTTCTCGCCCACCCGGGCTCGATCCCTCGCGAGTTGGT
 2501 TCAGCTGCTGCGTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
 2551 AAATCCGTCGGCATCCAGGAAACCGAGCAGCGGCTATCCGCGCATCCATGC
 2601 CCCCGAACTGCAAGGAGTGGGGAGGCACGATGCCGCTTGGTCGAGGGGG
 2651 ATCCTAGAACTAGCGAAAATGCAAGAGCAAGACGAAAACATGCCACACA
 2701 TGAGGAATACCGATTCTCTCATTAACATATTGAGCTGAGTTATCTGGGCT
 2751 TAAAGCAGAAGTCCAACCCAGATAACGATCATATAACATGGTTCTCCA
 2801 GAGGTTCATTAAGTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCTG

Figure 10b

2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTGAAGCTCCAATACATTGGC
2901 CACCTGATGCCAAGAACTGACTCATGTGATAAGACCCCTGATACTGGGAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTGAGCAAGCTTCAGGAGTTGGTA
3051 ATGGGCAGGGAAAGCCTGGCGTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGAACGTGACTGAACGTGATAGTGTAACTCCATGGTACAGA
3151 ATATAGGATAAAAAGAGGAAGAGTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTAGAATACCTTAGTTAGTTGAAAGTCTAAATTATTTACT
3251 TAGGATGGTACCCACTGCAATATAAGAAATCAGGCTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATAACCGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATAACCAATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTGAGAAGCCTTAAAGCTCAGGTCAGAATCTGTTTATA
3451 ATGTTCCAGGACACTGATCTAAAGCTCAGGTCAGAATCTGTTTATA
3501 GGCTCTAGGTGTATATTGTTGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTCGATCCCTGGCTTGGGAAAGAT
3601 CCCCTGGAGAAGGAAATGCCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGGAGCTGTAAAGCTACAGTCATGGGATTGCAAAGAG
3701 TTGAACACAACGTGAGCAACTAACGACAGCACAGTACAGTATACACCTGTG
3751 AGGTAGTGAAGTGAAGGTCAATGCAAGGGTCTCTGCATTGAGAAAAG
3801 ATTCTTACCATCTGAGCCACAGGGAAAGCCAAAGAATACTGGAGTGGG
3851 AGCCTATTCCCTCTCAGGGATCTCCATCCAGGAATTGAACTGGAG
3901 TCTCTGCATTTCAGGTGGATTCTCACCGAGCTGAACCTACAGGTGGATA
3951 CTACTCCAATATAAAGTGTAAAGTCCAGTTTCCCACCTTCCCAA
4001 AAGGTTGGGTCACTCTTTAACCTCTGTGGCCTACTCTGAGGCTGT
4051 TACAAGCTTATATATTTATGAAACACATTATTGCAAGTTGTTAGTTTAG
4101 ATTACAAATGTGGTATCTGGCTATTAGTGGTATTGGTGGTTGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTT
4201 TCAAGTTCTCATTGGTAAAGAATAGAAAGTCTCTGGATCTAAGTTATA
4251 GTGATTCTCAGTCTGTGGTCAATTCTATTCTACTCCTGCACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTGTTGGGCTTGTACATGGCTGGATTGG
4351 AGTGGGCCATGACATATGTTCTGGGACTGTGGCATGTGATGACATACACC
4401 GACAAGTGCCAGCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCACATTCTGCATGCTCTAGGGGGAAAGGGGGAAAGCTCGGTAT
4501 AGAACCTTTATTGTATTCTGATTGCCACTCTTATATTGCCCTTCA
4551 GCCCTTCTTGTCTCAAGTAACAGAGACAGTGTCTCCAGAACCAAC
4601 CCTACAAGAACAAAGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTGAACTCTTCTGGCCAGAGAACAAACCTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTCTGTCTGGCATGACCAGTCTCTCTTCAATTCTCTTCTAGA
4801 TGTAGGGCTTGTGACCAAGAGGCCCTGAGGCTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGTGCTTCATTCTCAGGTCTTGGGGGGGGGGGGGG
4901 GAGCTCGGTACCCGGGATCTCGACGGGATCCGATTACTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCAACATCTACACCAACACCGCT
5001 CGACCAAGGGTGAAGATATCGGCCGGGAGCGCGGGTGTAAATTACAAGCG
5051 AGATCCGATTACTACTGGCAGGTGCTGGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACCGCGGCGGTGGAATTACAAGCGAGATCCCCGGGAATTCAAGGACCTA
5201 CCATGGGATGGAGCTGTATCATCCTCTCTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACACTGGGGAGAGCGGGTGGAGGTGTGCAACC
5301 TGGCCGGTCCCTGCCTGCGCTGTCCGATCTGGCTTCAATTTCACCA
5351 CATATTGGATGAGTTGGTGAAGACAGGCACCTGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCAACAGATAGCAGTACGATTAACATATGGCCGTCTCT
5451 AAAGGATAGATTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTGGGCA
5551 AGCCCTTACTTCGGCTTCCCTGGTTGCTTATTGGGGCCAAGGGACCCC
5601 GGTCAACCGTCTCCACGCCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGGCCCTGGCTGCC
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTGTTGAACTCAGGCC
5751 CCTGACCAAGGGCGTGCACACCTTCCCGCTGTCCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACC
5851 CAGACCTACATCTGCAACGTGAATACAAGCCAGCAACACCAAGGTGG
5901 CAAGAGAGTTGAGCCAAATCTTGACAAAACTCACACATGCCACCGT

Figure 10c

5951 GCCCAGCACCTGAACTCCCTGGGGGACCGTCAGTCTTCCCTTCCCCC
6001 AAACCCAAGGACACCCCTCATGATCTCCCGAACCCCTGAGGTCAACATGGTACG
6051 GGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACG
6101 TGGACGGCGTGGAGGTGCAATAATGCCAAGACAAAGCCGGGGAGGAGCAG
6151 TACAAACAGCACGTACCGTGTGGTCAGCGTCCCTCACCGTCTGCACCAAGGA
6201 CTGGCTGAATGCCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCC
6251 CAGCCCCCATCGAGAAAACCATCTCAAAGCCAAGGGCAGCCCCGAGAA
6301 CCACAGGTGTACACCCCTGCCCGGATCCCGGGAGGAGATGACCAAGAACCA
6351 GGTCAAGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401 TGGAGTGGGAGGAGCAATGGGAGCGAGAACAACTACAAGACACGCCT
6451 CCCGTGCTGGACTCCGACGGCTCCTTCTTCTATAGCAAGCTCACCGT
6501 GGACAAGGAGCAGGTGGCAGGGGAACGTCTTCATGCTCCGTGATGC
6551 ACGAGGCTCTGCACAACCAACTACACGCAGAAGAGCCTCTCCGTCTCCC
6601 GGGAAATGAAAGCGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTA
6651 CTGGCGAAGCCGCTTGAATAAGCCGGTGTGCGTTGTCTATATGTTA
6701 TTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCCCGAAACCTGG
6751 CCCGTCTTCTTGTACGAGCATTCTAGGGGTCTTCCCTCTGCCAAAG
6801 GAATGCAAGGCTGTGAATGTGTGAAGGAACAGTTCTCTGGAAAGCT
6851 TCTGAAAGACAACACCGTGTAGCCACCCCTTGAGGCCAGGGAAACCC
6901 CCCACCTGGCGACAGGTGCCCTCGGCCAAAAGCCACGTGTATAAGATA
6951 CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTGTGAGTTGGATAGTT
7001 GTGAAAGACTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAA
7051 GGATGCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGCTCGGT
7101 GCACATGCTTACATGTGTTAGTCAGGTTAAAAAAACGCTAGGCCCC
7151 CCCAACACGGGAGCTGTTTCTTGTGAAAACACGATGATAATATGG
7201 CCTCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAG
7251 GCCGACATCCAGTCACCCAGAGGCCAACAGCAGCTGAGGCCAGCGTGG
7301 TGACAGACTGACCATCACCTGTAAGCCAGTCAGGATGTGGTACTTCTG
7351 TAGCCTGGTACCAAGCAGAAGCCAGGTAAAGGCTCAAAGCTGCTGATCTAC
7401 TGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAAGCGGTAGCGG
7451 TAGCGGTACCGACTTCACCTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501 TCGCCACCTACTACTGCCAGCAATAAGCCTATCGGTGTTGGCCAA
7551 GGGACCAAGGTGAAATCAAACGAACGGTGCACCATCTGCTTCTCAT
7601 CTTCGGCCATCTGATGAGCAGTTGAAATCTGAAACTGCCCTGTGTTG
7651 GCTGCTGATAAATCTATCCCAGAGGGCCAAGTACAGTGGAAAGGTG
7701 GATAACGCCCTCAATGGGTAACTCCCAAGGAGGTGTACAGAGCAGGA
7751 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAG
7801 CAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGC
7851 CTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTAGAGATC
7901 CCCCGGGCTGCAAGGATTGATATCAAGCTTATCGATAATCAACCTCTGG
7951 ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAAACTATGTTGCTCT
8001 TTACGCTATGTTGACGCTGTTAATGCCCTTGTATCATGCTATTGC
8051 TTCCCGATGGCTTCTATTTCTCTCTGTGTTGATTAATCTGGTTGCTGT
8101 CTCTTATGAGGAGTTGTTGCCGCTGTCAGGCAACGTGGCTGGTGTG
8151 ACTGTGTTGCTGACGCAACCCCCACTGGTGGGCAATTGCCACCCACTG
8201 TCAGCTCTTCCGGGACTTCGTTCCCCCTCCCTATTGCCACGGCGG
8251 AACTCATGCCGCTGCTTGGCCGCTGCTGGACAGGGCTCGCTGTTG
8301 GGCACATGACAATTCCGGTGGTGTGTCAGGGAAATCATGTCCTTCTCTG
8351 GCTGCTGCCCTGTTGCCACCTGGATTCTGCCGGGACGTCCTTCTGCT
8401 ACGTCCCTCGGCCCTCAATCCAGGGACCTTCTCCGCCCTGCTG
8451 CCGGCTCTGCCCTTCCGCGTCTCGCCCTGCCCTCAGACGAGTCG
8501 GATCTCCCTGGGCCCTCCCCCTGATCGATACCGTCAACATCGAT
8551 AAAATAAAAGATTATTTAGTCTCCAGAAAAGGGGGAAATGAAAGACC
8601 CCACCTGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCA
8651 TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAAGGAAC
8701 AGATGGAACAGCTGAATATGGGCAAAACAGGATATCTGTTGAGCAGTT
8751 CCTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCA
8801 AACAGGATATCTGTTGTAAGCAGTCTCTGCCCGCTCAGGGCAAGAAC
8851 AGATGGTCCCAGATGCCGTCAGCCCTCAGCAGTTCTAGAGAACCATC
8901 AGATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCCTGTCCTTATT
8951 GAACTAACCAATCAGTCGCTTCGCTCTGTCGCGCCTCTGCTCC
9001 CCGAGCTCAATAAGAGGCCACAACCCCTACTCGGGGCCAGTCCTC

Figure 10d

9051 CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCTCTTGCA
9101 GTTGCATCCGACTTGTGGTCTCGCTGTTCTGGGAGGGTCTCCTCTGAG
9151 TGATTGACTACCCGTCAGCGGGGGTCTTCATT

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

1 GATCAGTCCTGGTGGTCATTGAAAGGACTGATGCTGAAGTGAAGCTCC
 51 AATACTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCTG
 101 ATACTGGAAAGATTGAAGGCAGGGAGAAGGGATGACAGAGGATGGAA
 151 GAGTTGGATGGAATCACCACACTCGATGGACATGAGTTGAGCAAGCTTC
 201 AGGAGTTGGTAATGGGCAGGGAAAGCCTGGCGTGCAGTCATGGGTT
 251 GCAAAGAGTTGGACACTACTGAGTGACTGAACGTGATAGTGTAACTC
 301 CATGGTACAGAATATAGGATAAAAAGAGGAAGAGTTGCCCTGATTCTG
 351 AAGAGTTGTAAGGATATAAAAGTTAGAATACCTTAGTTGAGTCTTA
 401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTT
 451 AGAGACTGATGAGAGAAATGAGCCTGGCATACCAGAACGTAACAGCT
 501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATTGGTTATATA
 551 GCATGAAGCTGATGCCAGCAATTGAAGGAACCATTTAGAAACTAGTATC
 601 CTAAACTCTACATGTTCCAGGACACTGATCTAAAGCTCAGGTTCAGAAT
 651 CTTGTTTATAGGCTCTAGGTGATATTGTGGGGCTTCCCTGGTGGCTCA
 701 GATGGTAAAGTGTGCTGCAATGTGGGTGATCTGGGTTGATCCCTGG
 751 CTTGGGAAAGATCCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
 801 ACCTGGAAAATTCCATGGACAGGGAGCTGTAAGCTACAGTCCATGGG
 851 ATTGCAAAGAGGTGAACACAACACTGAGCAACTAAAGCACAGCACAGTACAGT
 901 ATACACCTGTGAGGTTGAAGTGAAAGGTTCAATGCAGGGCTCCTGC
 951 ATTGCAGAAAGATTCTTACCATCTGAGGCCACCAAGGGAAAGCCAAGAATA
 1001 CTGGAGTGGGTAGCCCTATCCCTCCAGGGGATCTTCCATCCCAGGAA
 1051 TTGAACTGGAGTCTCCTGCATTCAGGTGGATTCTCACCAAGCTGAACTA
 1101 CCAGGTGGATACTACTCCAATATTAAAGTCTTAAAGTCCAGTTTCCA
 1151 CCTTCCCAAAAAGGTTGGGCACTCTTTAACCTCTGTGGCTACT
 1201 CTGAGGCTGCTCTAACGCTTATATTTGAAACACATTATTGCAAGTT
 1251 GTAGTTTATGATTTACATGTTGATCTGGCTATTAGTGGTATTGGTG
 1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
 1351 ATACACACTTTCAAGTTCTCATTGGTGAAAATAGAAAGTCTCTGGAT
 1401 CTAAGTTATATGTGATTCTCAGTCTGTGGTCAATTCTATTCTACTCC
 1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTGTTGTTCA
 1501 TGCCCTGGGTGAGTGGGCATGACATATGTTCTGGGCTTGTACATGGC
 1551 TGATTGGTGGACAAGTGGCAGCTGATCTGATCTGGGACTGTGGCATGTGA
 1601 TGACATACACCCCTCTCCACATTCTGCATGTCCTAGGGGGAAAGGGGG
 1651 AAGCTGGTATAGAACCTTATTGTATTCTGATTGCTCACTTCTTAT
 1701 ATGCCCTCATGCCCTTCTTGTCTCAAGTAACCAAGAGACAGTGCTTC
 1751 CCAGAACCAACCTACAAGAAACAAAGGGCTAAACAAAGCCAATGGGAA
 1801 GCAGGATCATGGTTGAACCTTTCTGGCCAGAGAACAAACACCTGCTATG
 1851 GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
 1901 AGCTGGCAGGCTCAGCGTTCTGCTTGGCATGACCAAGTCTCTCTTCATT
 1951 CTCTTCTAGATGTAGGGCTTGGTACCGAGGCCCCGTAGGGCTTCTGCA
 2001 GAATATAATATGAAACTGAGTGTGATGCTTCATTTCAGGTTCTGGGG
 2051 GCGCGAATTGAGCTGGTACCCGGGATCTGACGGATCCGATTACTT
 2101 ACTGGCAGGTGCTGGGGCTTCCGAGACAATCGCGAACATCTACACCA
 2151 CAACACCGCCTCGACCAGGGTGAAGATACGGCCGGGACGGGGCGGTGGT
 2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGCTTCCGA
 2251 GACAATCGCGAACATCTACACCAACACACCCGCTCGACCCAGGGTGA
 2301 TATGGCCGGGAGCGGGCGGTGGTAATTACAAGCGAGATCTGAGAAC
 2351 TTGTTGGGAATTCAAGGACATCGATCCCGCCGCCCCACATGGAAATGGAGCTG
 2401 GGTCTTCTCTCTCCGTCAAGTAACACTACAGGTGTCCACTCCGACATCC
 2451 AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
 2501 ACTATCACATGTCAGGCAAGTGGGAATTACAAATTATTAGCATGGTA
 2551 TCAGCAGAACAGGGAAAATCTCTCAGCTCTGGTCTATAATGCAAAA
 2601 CCTTAGCAGATGGTGTGCCATCAAGGTTCAAGGGTCAAGTGGGATCAGGAACA
 2651 CAATATTCTCTCAAGATCAACAGCCTGAGGGTGAAGATTGGGAGTTA
 2701 TTACTGTCAACATTGGAGTACTCCGTGGACGTTGGTGGAGGGCACCA
 2751 AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCA
 2801 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCTCAGTCGTGCTTCTT

Figure 11b

2851 GAACAACCTCTACCCCAAAGACATCAATGTCAGTGGAAAGATGATGGCA
2901 GTGAACGACAAATGGCGTCTGAACAGTTGGACTGATCAGGACAGCAAA
2951 GACAGCACCTACAGCATGAGCAGCACCCCTCACATTGACCAAGGACGAGTA
3001 TGAACGACATAACAGCTATACTGTGAGGCCACTCACAAGACATCAACTT
3051 CACCCATTGTCAAGAGCTCAACAGGAATGAGTGTGAAAGCATCGATTT
3101 CCCCTGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAA
3151 GCGCCTTGAATAAGGCCGTGCGTTGTCTATATGTTATTTCCACC
3201 ATATTGCCGTCTTGGCAATGTGAGGGCCGAAACCTGGCCCTGTCTT
3251 CTTGACGAGCATTCTAGGGTCTTCCCTCTCGCCAAGGAATGCAAG
3301 GTCCTGAAATGCTGTAGCGACCTTGCAGGCAGCGAACCCCCCACCTGG
3351 CAAACAACGCTGTAGCGACCTTGCAGGCAGCGAACCCCCCACCTGG
3401 CGACAGGTGCCCTTGCGGCCAAAAGCCACGTGTATAAGATAACACCTGAA
3451 AGGGGGCACAACCCCAGTCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501 GTCAAATGGCTCTCTCAAGCTTCAACAAGGGCTGAAGGGATGCCA
3551 GAAGGTACCCCATGATGGGATCTGATCTGGGCTCGGTCCACATGCT
3601 TTACATGTGTTAGTCGAGGTAAAAAAACGTCTAGGCCCCCGAACAC
3651 GGGGACGTGGTTCTTCTGGTAGGCATCTTCCATGCCACCCAGGCCAGGGTT
3701 TCTCTGCTCTGGTAGGCATCTTCCATGCCACCCAGGCCAGGGTT
3751 CAGCTCAGCAGTCTGGGGCAGAGCTGTGAAGGCCAGGGCTCAGTC
3801 GTTGTCTGCACAGCTCTGGCTTCAACATTAAGACACCTTATGCACT
3851 GGGTGAAGCAGAGGCCCTGAACAGGGCTGGAGTGGATTGGAAGGATTGAT
3901 CCTCGAATGGAATACTGAATATGACCCGAAGTCCAGGGCAAGGCCAC
3951 TATAACAGCAGACACATCCTCAACACAGTCACCTGCAGCTCAGCAGCC
4001 TGACATCTGAGGGACACTGGCTCTATTACTGTGCTAGTGGAGGGAACTG
4051 GGGTTCTTACTGGGCAAGGGACTCTGGTCACTGTCTGCAGCCAA
4101 AACGACACCCCCATCTGTCTATCCACTGGGCTGGATCTGTCAGCCAAA
4151 CTAACCTCATGGTGACCCCTGGGATGCCTGGTCAAGGGTATTCCCTGAG
4201 CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251 CTTCCCAGCTGCTCTGCAGTTGACCTCTACACTGTGAGCAGCTCAGTGA
4301 CTGTCCTCCAGCACCTGGCCAGCGAGACCGTCACCTGCACAGCTTGC
4351 CACCCGGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCAGGGATTG
4401 TACTGTGGAGGTGGAGGTAGGCCACCATCACCATTAAATCTAGAG
4451 TTAAGGGGCCCTCGAGATCTGACATCGATAATCAACCTCTGGATTACAA
4501 AATTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCTTTACGC
4551 TATGTGGATACGCTGCTTAATGCCCTTGTATCATGCTATTGCTTCCCGT
4601 ATGGCTTCATTTCTCCCTTGATATAAATCTGGTTGCTGTCTTTA
4651 TGAGGAGTTGTGGCCCGTGTCAAGGCAACGTGGCGTGGTGTCACTGTG
4701 TTGCTGACGCAACCCCCACTGGTTGGGCATTGCCACCCCTGTCACTC
4751 CTTTCCGGGACTTTGCGCTTCCCCCTCCCTATTGCCACGGGGAAACTCAT
4801 CGCCGCCCTGCTTGGCCCTGCTGGACAGGGGCTCGGCTGTGGGACTG
4851 ACAATTCCGTGGTGTGTCGGGGAAATCATGCTCTTCCCTGGCTGCTC
4901 GCCTGTGTTGCCACCTGATTCTGCCGGGACGTCTTCTGCTACGTCCC
4951 TTCCGGCCCTCAATCCAGCGGACCTTCTTCCCGGGCTGCTGCCGGCTC
5001 TGCGGCCCTTCCCGCTTCCCGCTGATCGATAAAATAAAGATTATTAGT
5051 CTTGGGGCGCTCCCCCGCTGATCGATAAAATAAAGATTATTAGT
5101 CTCCAGAAAAGGGGGAAATGAAAGACCCCCACCTGTAGGTTGGCAAGCT
5151 AGCTTAAGTACGCCATTGCAAGGCATGGAAAAAAATACATAACTGAGAA
5201 TAGAGAAGTTAGATCAAGGTCAAGGAACAGATGGAACAGCTGAATATGGG
5251 CCAAAACAGGATATCTGGTAAGCAGTTCTGCCCGCTCAGGGCAAG
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGGTAAGCA
5351 GTTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCCGGTCC
5401 AGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGGCCCAA
5451 GGACCTGAAATGACCCCTGTGCCTTATTGAACTAACCAATCAGTTCGCTT
5501 CTCGCTCTGTTGCCGCTTCTGCTCCCCGAGCTCAATAAAAGAGGCCA
5551 CAACCCCTCACTCGGGGCCAGTCTCGATTGACTGAGTCGCCGGGT
5601 ACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTC

Figure 11c

5651 GCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701 GGTCTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

Figure 12a
SEQ ID NO:9
LSNRL Vector

1 TTTGAAAGACCCACCCGTAGGTGCGAAGCTAGCTTAAGTAACGCCACTT
51 TGCAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTCAGATCAAG
101 GTCAGGAACAAAGAAACAGCTGAATACCAACAGGATATCTGTGGTAAGC
151 GGTTCCTGCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201 GGCACAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCGGGGCCA
251 AGAACAGATGGTCCCCAGATGCGGCCAGCAGTTCTAGTGA
301 TCATCAGATGTTCCAGGGTGCCAACAGGACCTGAAAATGACCCCTGTACC
351 TTATTTGAACTAACCAATCAGTCGTTCTCGCTTCTGTTCGCGCCTTC
401 CGCTCTCGAGCTCAATAAAAGAGGCCAACACCCCTCACTCGGCGCGCCA
451 GTCTTCCGATAGACTGCCCGGGTACCCGATTCCCAATAAGCCT
501 CTGCTGTTGATCCGAATCGTGGTCTCGCTGTTCTGGAGGGTCTC
551 CTCTGAGTGAATTGACTACCCACGACGGGGTCTTCATTGGGGGCTCGT
601 CCGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCCACGGGAGG
651 TAAGCTGCCAGCAACTTATCTGTGTCTGCCATTGTCTAGTGTCTATG
701 TTTGATGTTATGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751 CTGGCGGACCCGTGGTGAACGTGACGGAGTTCTGAACACCCGGCGAACCTGA
801 CTGGGAGACGCTCCAGGGACTTTGGGGCCGTTTGTGGCCCGACCTGA
851 GGAAGGGAGTCGATGTGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901 AGGAGACGAGAACCTAAACACTTCCCGCTCCGCTGAATTGGTTCTGGT
951 CGGTTGGAACCGAAGCCGCGCTTGTCTGCTGAGCAAGCTGGC
1001 TCGAGGTGAGGACTGGGACCCCTGCACCGAACATGGAGAACACAACATC
1051 AGGATTCTAGGACCCCTGCTGTACAGGGGGTTTTCTTGTGA
1101 CAAGAACCTCACAATACCACAGAGTCAAGACTCGTGTGGACTTCTCTC
1151 AATTTCTAGGGGAGCACCCACGTGCTGGCAAAATTGCGAGTCCCC
1201 AACCTCCAATCACTCACCAACCTCTGTCTGGCAATTGTCTGGCTATC
1251 GCTGGATGTCGCGGGGTTTATCATATTCTCTCATCCTGCTGCTA
1301 TGCTCATCTTGTGGTCTCTGGACTACCAAGGTATGTTGCCGT
1351 TTGCTCTACTTCCAGAACATCAACTACCAAGCACGGGACCATGCAAGA
1401 CCTGCACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTGTTGCTGT
1451 ACAAAACCTCGGACGAAACTGCACCTGTTATCCCATCCCATCCTG
1501 GGCTTCGCAAGATTCTATGGGAGTGGGCTCAGTCCGTTCTCCTGGC
1551 TCAGTTTACTAGTGCCTTGTGGACTACCAAGGTATGTTGCCGT
1601 GTTGGCTTCAAGTTATGGATGATGTTGTTGGGCTTGGGCTTGGCT
1651 CAACATCTTGAGTCCCTTTACCTCTATTACCAATTTCCTTGTCTT
1701 GGGTATACATTAAACCTAATAAAACCAACGTTGGGGCTACTCCCTTA
1751 ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTACCGCAAGAACAT
1801 ATTGTACTAAAAATCAAGCAATGTTGCCAAACTGCTGTAAATAGACC
1851 TATTGATTGAAAGTATGTCAGAGACTTGTGGCTTTGGGTTTGCTG
1901 CCCCTTTACACAATGTGGCTATCTGCCTTAATGCCTTATATGCATGT
1951 ATACAATCTAAGCAGGGTTTCACTTCTCGCCAACCTACAAAGGCTTCT
2001 GTGTAACAAATCTGAACCTTACCCCGTGGGCTTGGCT
2051 TCTGCCAAGTGTGCTGACGCCAACCCCACTGGATGGGCTTGGCTATC
2101 GGGCATAGCCGATGCCGGACCTTGTGGCTCTCGCCGATCCATACT
2151 GCGGAACCTCTAGCAGCTGTTGCTCGCAGGGCTGGAGCGAAACT
2201 TATGGCACCGACAACCTGTGTCCTCTCGGAAATACACCTCTTTC
2251 CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCTCAGGATATAGTAGT
2301 TTCGCTTGTGATAGGGAGGGGAAATGTAAGCTTATGCAATACACTTGT
2351 AGTCTGCAACATGGTAACGATGAGTTAGCAACATGCCCTACAAGGAGAG
2401 AAAAGCAGCTGCGATGCCGATGGTGGAGTAAGGTGGTACGATGTGC
2451 CTTATTAGGAAGGCAACAGACAGGCTGACATGGATGGAGCAACACTG
2501 AATTCCGCATTGCGAGATAATTGTATTAAAGTGCCTAGCTGATAACAGC
2551 AAACGCCATTGGACCATTCACCAACATTGGTGTGCACCTTCCAAAGCTT
2601 CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651 ACGTAGAAAGCCAGTCGCAGAACGGCTGACCCGGATGAATGTCA
2701 CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751 TAGCTTGCAAGTGGCTACATGGCAGTAGCTAGACTGGGCGTTTATGG
2801 ACAGCAAGCGAACCGAATTGCCAGCTGGGCGCCCTGGTAAGGTGG

Figure 12b

2851 GAAGCCCTGCAAAGTAAACTGGATGGCTTCTTGGCCCAAGGATCTGAT
2901 GGGCAGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTCGC
2951 ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGTTGGGTTGGA
3001 GAGGCTATTGGCTATGACTGGGACAACAGACAATCGGCTGCTGATG
3051 CCGCCGTGTTCCGGCTGTCAGCGCAGGGCGCCGGTTCTTTGTCAG
3101 ACCGACCTGTCGGTGCCTGAATGAACACTGCAGGACGAGGCAGCGCGCT
3151 ATCGTGGCTGGCACGACGGCGTCCCTGCGCAGCTGCTGACGTTG
3201 TCAGTAAGCGGAAGGGACTGGTGTATTGGCGAAGTGCCGGGAG
3251 GATCTCTGTCACTCACCTGCTCTGCGAGAAAGTATCCATCATGGC
3301 TGATGCAATGGCGGGCTGACATCGCTGATCCGCTACCTGCCATTG
3351 ACCACCAAGCGAACATCGCATCGAGCGAGCACGTAACCGGATGGAAGCC
3401 GGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGCGCC
3451 AGCCGAACGTTCGCCAGGCTAAGGCAGCGATGCCGACGGCGAGGATC
3501 TCGCGTACCCATGGCGATGCGCTGCTTGCGAATATCATGGTGGAAAAT
3551 GGCCTTTCTGGATTATCGACTGTGGCGGCTGGGTGTGGCGGACCG
3601 CTATCAGGACATAGCGTGGCTACCCGATATTGCTGAAGAGCTTGGG
3651 GCGAATGGGCTGACCGCTTCTCGTGTACGGTATCGCCGCTCCCGAT
3701 TCGCAGCGCATGCCCTCATGCCCTTGTACGAGTTCTCTGAGCGGG
3751 ACTCTGGGTTGCAAATGACCGACCAAGCGACGCCAACCTGCCATCAC
3801 AGATTCGATTCCACGCCCTCTATGAAAGGGTGGGCTTCGGAATCG
3851 TTTCCGGGACGCCGGCTGGATGATCCCTCAGCGCGGGGATCTCATGCTG
3901 GAGTTCTGCCACCCCAACCCCTGGCTATTATTGGGTGGACTAACCA
3951 TGGGGGAATTGCCGTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
4001 ACTCAGCAATTCCAGCAGCTCAAGCCCGAGTACAGGATGATCTCAGGG
4051 GGTGAAAATCAATCTCTAACCTAGAAAAGTCTCTACCTCCCTGCTG
4101 AAGTTGTCCTACAGAATCGAAGGGCCTAGACTTGTATTCTAAAAGAA
4151 GGAGGGCTGTGCTCTAAAAGAAGATGTTGCTTCTATGCCGACCA
4201 CACAGGACTAGTGAGAGACAGCATGCCAATTGAGAGAGAGGGCTTAATC
4251 AGAGACAGAAAATGTTGAGTCACACTCAAGGATGTTGAGGGACTGTT
4301 AACAGATCCCCTGGTTTACACCTTGATATCTACCATTATGGGACCCCT
4351 CATGTAACCTCAATGATTTGCTCTCGGACCCCTGATTCTAATCGAT
4401 TAGTCCAATTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTT
4451 ACTCAACAATATCACCAGCTGAAGCCTATAGACTACAGGCCATAGATAAA
4501 ATAAAAGATTTATTAGTCTCCAGAAAAGGGGGATGAAAGACCCCA
4551 CCTGAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGG
4601 AAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTAGGAACAGA
4651 TGGAACAGCTGAATATGGCCAAACAGGATATCTGGTAAGCAGTTCC
4701 GCCCGGCTCAGGCCAAGAACAGATGGAACAGCTGAATATGGCCAAAC
4751 AGGATATCTGGTAAGCAGTCTCTGCCGGCTCAGGCCAAGAACAGA
4801 TGGTCCCCAGATGCGGTCCAGGCCCTCAGCAGTTCTAGAGAACCATCAGA
4851 TGGTCCAGGGTGCCCAAGGACCTGAAATGACCCCTGTCCTTATTGAA
4901 CTAACCAATCAGTTCGCTCTCGCTCTGTCGCGCTCTGCTCCCCG
4951 AGCTCAATAAAAGAGCCCCACAACCCCTCACTGGGGGCCAGTCCTCCGA
5001 TTGACTGAGTCGCCCGGGTACCCGTGATCCAATAAAACCTCTTGCAGTT
5051 GCATCCGACTGTGGTCTCGCTTCTGGGAGGGTCTCCTCTGAGTGA
5101 TTGACTACCCGTCAGCGGGGGCTTCTTATT

1 - 589 MoMuSV 5' LTR
659 - 897 Retroviral packaging region
1034 - 1714 Hepatitis B surface antigen
2279 - 2595 RSV promoter
2951 - 3745 Neomycin phosphotransferase gene
4537 - 5130 MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc49IL2 Vector

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
 51 AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCCTG
 101 ATACTGGGAAAGATTGAAGGCAGGAGAGAAGGGATGACAGAGGATGGAA
 151 GAGTTGGATGGAAATCACCACACTCGATGGACATGAGTTGAGCAAGCTCC
 201 AGGAGTTGGTAATGGCGAGGAAAGCCTGGCGTCTGCAGTCCATGGGGTT
 251 GCAAAGAGTTGGACACTACTGAGTGAACGTGAACTGATAGTGTAACTC
 301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGGTTGCCCTGATTCTG
 351 AAGAGTTGAGGATATAAAAGTTAGAATACCTTAGTTGAAAGTCTTA
 401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
 451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
 501 ATTGGTTATAGCTGTTATAACCAATATAACCAATATATTGGTTATATA
 551 GCATGAAGCTTGTATGCCAGCAATTGAGGAACCATTTAGAACTAGTATC
 601 CTAACACTACATGTTCCAGGACACTGATCTAAAGCTCAGGTTCAGAAT
 651 CTTGTTTATAGGCTTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
 701 GATGGTAAAGTGTCTGCTGCAATGTGGGTGATCTGGGTTGATCCCTGG
 751 CTTGGGAAGATCCCTGGAGAAGGAATGGCAACCCACTCTAGTACTCTT
 801 ACCTGGAAAATCCATGGACAGAGGAGCCTGTAAGCTACAGTCCATGGG
 851 ATTGCAAAGAGTTGAACACAACGTGAGCAACTAACGACAGCACAGTACAGT
 901 ATACACCTGTGAGGTGAAGTGAAGGTTCAATGCAGGGCTCCTGC
 951 ATTGCAAGAAAGATTCTTACCATCTGAGGCCACCGGGAAAGCCAAGAATA
 1001 CTGGAGTGGGTAGCCTATTCTCCTCCAGGGGATCTTCCCCTCCAGGAA
 1051 TTGAACCTGGAGTCTCCTGCATTTCAGGTGGATTCTCACCAAGCTGAAC
 1101 CCAGGTGGATACTACTCCAATATTAAGTGTCTAAAGTCCAGTTTCCC
 1151 CCTTCCCAAAAAGGTTGGTCACTCTTTAACTTCTGTGGCCTACT
 1201 CTGAGGCTGTCTACAAGCTTATATATTATGAACACATTATTGCAAGTT
 1251 GTTAGTTTAGATTTACAATGTGGTATCTGGCTATTAGTGGTATTGGTG
 1301 GTTGGGGATGGGGAGGGTGTAGCATCTCAGAGGGCAGCTAGATACTGTC
 1351 ATACACACTTTCAAGTTCTCATTGGTAAAGTAAAGTCTCTGGAT
 1401 CTAAGTTATATGTGATTCTCAGTCTGTGGTCAATTCTATTCTACTCC
 1451 TGACACTCAACAAGGAAACAGATATCAAGGGACACTTGTGTTGTTCA
 1501 TGCCCTGGGTGAGTGGGCATGACATATGTTGGCCTTGTACATGGC
 1551 TGATTGGTGGACAAGTGCAGCTGTGATCCTGGACTGTGGCATGTGA
 1601 TGACATACACCCCTCTCCACATTCTGCATGTCCTAGGGGGAAAGGGGG
 1651 AAGCTCGGTATAGAACCTTATTGTATTCTGATTGCCTCACTTCTTAT
 1701 ATTGCCCCCATGCCCTCTTGTCTCAAGTAACCCAGAGACAGTGCCTC
 1751 CCAGAACCAACCCCTACAAGAAACAAAGGGCTAACAAAGCCAAATGGGA
 1801 GCAGGATCATGGTTGAACCTCTCTGGCCAGAGAACAAATACCTGCTATG
 1851 GACTAGATACTGGGAGAGGAAAGGAAAGTAGGGTGAATTATGGAAGGA
 1901 AGCTGGCAGGCTCAGCCTTCTGTCTGGCATGACCAGTCTCTTCTCATT
 1951 CTCTCTAGATGTAGGGCTTGGTACCAAGAGCCCTGAGGCTTCTGCA
 2001 GAATATAAAATATGAAACTGAGTGTATGCTTCCATTTCAGGTTCTGGG
 2051 GCGCCGAATTGAGCTGGTACCCGGGGATCTCGAGAAGCTTAACCATG
 2101 GAATGGAGCTGGCTTCTCTCTCTGTCACTGAAACTACAGGTGTCCA
 2151 CTCCCAAGGTTCACTGAGCAGTCTGACGCTGAGGTGGTGAACACCTGGG
 2201 CTTCAGTGAAGATTCTCTGCAAGGCTTCTGGCTACACCTCACTGACCAT
 2251 GCAATTCACTGGTGAAACAGAACCTGAACAGGGCTGGAAATGGATTGG
 2301 ATATTTCTCCGGAAATGATGATTTAAATACAATGAGAGGTTCAAGG
 2351 GCAAGGCCACACTGACTGCAGACAAATCTCCAGCACTGCCCTACGTGCA
 2401 CTCACAGCCTGACATCTGAGGATTCTGCAGTGTATTCTGTACAAGATC
 2451 CCTGAATATGCCCTACTGGGGTCAAGGAACCTCACTGCACGGCTGGACATT
 2501 GAGGGGGAGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
 2551 GTGATGTCAAGTCTCCATCTCCCTACCTGTGTCAGITGGCGAGAAGGT
 2601 TACTTGAGCTGCAAGTCCAGTCAGAGCCTTATATAGTGGTAATCAA
 2651 AGAACTACTTGGCCTGGTACCAAGAGAAACCAAGGGCAGTCTCCTAAACTG
 2701 CTGATTTACTGGGACATCGCTAGGAATCTGGGTCCCTGATCGCTTCA
 2751 AGGCAGTGGATCTGGGACAGATTCACTCTCCATCAGCAGTGTGAAGA
 2801 CTGAAGACCTGGCAGTTATTACTGTCAGCAGTATTAGCTATCCCCTC

Figure 13b

2851 ACCTTCGGTCTGGGACCAAGCTGGTCTGAAACGGGCCGAGCCCAA
2901 ATCTCCTGACAAAACCTCACACATGCCACCGTGCCTGACCTGAACCTCC
2951 TGGGGGGACCGTCAGTCTTCCCTTCCCCAAAACCCAAGGACACCCCTC
3001 ATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCA
3051 CGAAGACCCCTGAGGTCAAGTCAACTGGTACGTGACGGCGTGGAGGTGC
3101 ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151 GTGGTCAGCGTCTCACCCTGACCCAGGACTGGCTGAATGGCAAGGA
3201 GTACAAGTGAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAAA
3251 CCATCTCCAAAGCCAAGGGCAGCCCCAGAGAACACAGGTGTACACCCCTG
3301 CCCCCATCCGGATGAGCTGACCAAGAACCGGTGAGCCTGACCTGCCT
3351 GGTCAAAGGCTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401 GGCAGCCGGAGAACAACTACAAGACCAAGCCTCCCGTGTGGACTCCGAC
3451 GGCTCCTTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCA
3501 GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTGTGACAACC
3551 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGTAAAGGAGGCAGTCA
3601 GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAAC
3651 GGAGCATTACTGTGGATTACAGATGATTTGAATGGAATTAAATT
3701 ACAAGAATCCAAAACCTCAGGATGTCACATTAAAGTTTACATGCC
3751 AAGAAGGCCACAGAACTGAAACATCTCAGTGTCTAGAAGAAGAACTCAA
3801 ACCTCTGGAGGAAGTGCTAAATTAGCTCAAAGCAAAACTTCACTTAA
3851 GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACATAAG
3901 GGATCTGAAACAACATTATGTGTGAATATGCTGATGAGACAGCAACCAT
3951 TGTAGAATTCTGAACAGATGGATTACCTTTGTCAAAGCATCTCAA
4001 CACTAACTTGAAGCTGTAAACATCGATAAAATAAAAGATTATTAGT
4051 CTCAGAAAAAAGGGGGAAATGAAAGACCCACCTGTAGGTTGGCAAGCT
4101 AGCTTAAGTAACGCCATTGCAAGGCATGGAAAATACATAACTGAGAA
4151 TAGAGAAGTTCAGATCAAGGTCAAGGACAGATGAAACAGCTGAATATGGG
4201 CCAACAGGATATCTGTGTAAGCAGTCTGCCCGGCTCAGGGCAAG
4251 AACAGATGGAACAGCTGAATATGGCCAAACAGGATATCTGTGGAAGCA
4301 GTTCTGCCCCGGCTCAGGGCAAGAACAGATGGTCCCCAGATGCGGTCC
4351 AGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGGCCCAA
4401 GGACCTGAAATGACCCCTGTGCCTTATTGAACTAACCAATCAGTCGCTT
4451 CTCGCTTCTGTTCCGGCCCTCTGCTCCCCGAGCTAATAAAAGAGCCCA
4501 CAACCCCTCACTCGGGGGCCAGTCCTCGATTGACTGAGTCGCCGGGT
4551 ACCCGTGTATCCAATAAACCTCTTGCAGTTGCACTCCGACTGTGGTCTC
4601 GCTGTTCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGGG
4651 GGTCTTTCATT

1 - 2055 Bovine/human alpha-lactalbumin 5' flanking region

2098 - 4011 cc49-IL2 coding region

4068 - 4661 MoMuLV 3' LTR

Figure 14a
SEQ ID NO:11
Alpha-Lactalbumin YP Vector

1 GATCAGTCCTGGTGGTCAATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
 51 AATACTTTGGCCACCTGATGCGAAGAAGTCACTGACTCATGTGATAAGACCCCTG
 101 ATACTGGGAAAGATTGAAGGCAGGAGAGAAGGGATGACAGAGGATGGAA
 151 GAGTTGGATGGAATCACCACACTCGATGGACATGAGTTGAGCAAGCTTCC
 201 AGGAGTTGTAATGGCAGGGAGGCTGGCGTGCAGTCCATGGGTT
 251 GCAAAGAGTTGGACACTACTGAGTGACTGAACGTGATAGTGAATC
 301 CATGGTACAGAATATAGGATAAAAAGAGGAAGAGGTTGCCCTGATTCTG
 351 AAGAGTTGAGGATATAAAAGTTAGAATACCTTGTGAAAGTCTTA
 401 AATTATTTACTTAGGATGGTACCCACTGCAATAAAGAAATCAGGTT
 451 AGAGACTGATGAGAGAATGAGCCCTGGCATACCAAGAAGCTAACAGCT
 501 ATTGGTTAGCTGTTATAACCAATATAACCAATATAACCAATATTGGTTATATA
 551 GCATGAAGCTTGTGCGCACATTGAAAGGAACATTAGAACTAGTATC
 601 CTAACACTCATGTTCCAGGACACTGATCTAAAGCTCAGGTTCAGAAT
 651 CTTGTTTATAGGCTCTAGGTGTATATTGTGGGCTTCCCTGGCTCA
 701 GATGGTAAAGTGTCTGCCGCAATGTTGGGTGATCTGGGTCATCCCTGG
 751 CTTGGGAAAGATCCCCTGGAGAAGGAATGGCAACCCACTCTAGTACTCTT
 801 ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAAGCTACAGTCCATGG
 851 ATTGCAAAGAGTTGAACACAACGCAACTAAGCAGCACAGTACAGT
 901 ATACACCTGTGAGGTGAAGTGAAAGTCAATGCAAGGGTCTCCTGC
 951 ATTGAGAAGATTCTTACCATGTCAGGCCACAGGGAAAGCCAAGAATA
 1001 CTGGAGTGGGTAGCCTATCCTCTCCAGGGATCTTCCATCCCAGGAA
 1051 TTGAACTGGAGTCTCCTGCAATTTCAGGTGGATTCTCACCAAGCTGAAC
 1101 CCAGGTGGATACTACTCCAATATTAAAGTCTTAAAGTCCAGTTTCCCA
 1151 CCTTCCAAAAGGTTGGTCACTCTTTTAACCTTCTGTTGGCTACT
 1201 CTGAGGTGCTACAAGCTTATATTTATGAAACACATTATGCAAGTT
 1251 GTTAGTTAGATTACAATGTGGTATCTGGCTATTAGTGGTATTGGT
 1301 GTTGGGATGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
 1351 ATACACACTTTCAAGTCTCCATTGGTGAATAGAAAGTCTCTGGAT
 1401 CTAAGTTATATGTGATTCTCAGTCTGTGGTCATATTCTATTCTACTCC
 1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTGTTGTTCA
 1501 TGCCTGGGTGAGTGGCCATGACATATGTTCTGGCTTACATGGC
 1551 TGGATTGGTGGACAAGTGCCAGCTGATCTGGGACTGTGGCATGTGA
 1601 TGACATACACCCCTCTCCACATTGCACTGTCTAGGGGAAAGGGGG
 1651 AAGCTCGGTATAGAACCTTATTGTATTCTGATTGCTCACTTCTTAT
 1701 ATTGCCCCATGCCCCCTTCTGTTCTCAAGTAACCAAGAGACAGTCTTC
 1751 CCAGAACCAACCCCTACAAGAAACAAGGGCTAACAAAGCCAATGGGAA
 1801 GCAGGATCATGGTTGAACCTCTCTGGCCAGAGAACAAACCTGCTATG
 1851 GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
 1901 AGCTGGCAGGCTCAGCGTTCTGTCTGGCATGACCAAGTCTCTCTCATT
 1951 CTCTTCCCTAGATGTAGGGCTTGGTACCGAGGCGCTTGAGGCTTCTGCA
 2001 GAATATAAAATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTGGG
 2051 GCGCGAACATTGAGCTCGGACCCGGATCTGACGGATCCGATTACTT
 2101 ACTGGCAGGTGCTGGGCTTCCGAGACAATCGGAACATCTACACCACA
 2151 CAACACCGCTCGACCAGGGTGAGATATCGGCCGGGACGCCGGTGGT
 2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGCTTCCGA
 2251 GACAATCGCGAACATCTACACCACAAACCCCTCGACCAGGGTGAGA
 2301 TATCGGCCGGGACCGCGGGTGGTAATTACAAGCGAGATCTCGAGTTAA
 2351 CAGATCTAGGCCCTCTAGGTGACGGATCCCCGGGATTCCGGCGCC
 2401 CCATGATGCTTGTCTCTGCTCTGGTAGGCTACCTATTCCATGCC
 2451 ACCCAGGCCAGGTCCAACGCACTGCAAGCTGCTGGGCTGAGCTGGTGAAGCC
 2501 TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
 2551 GCTACTATTACACTGGGTAAGCAGAGGCCGGACAGGGACTTGAGTGG
 2601 ATTGCATGGATTATCTGGAAATGTATTACTACGTACAATGAGAAGTT
 2651 CAAGGGCAAGGCCACACTGACTGCAAGACAAATCTCCAGCACAGCCTACA
 2701 TGCACTCAACAGCCTGACCTCTGAGGACTCTGGGTCTATTCTGTGCA
 2751 AGGGGTGACCATGATCTGACTCTGGGCAAGGCACCAACTCTCACAGT
 2801 CTCCCTAGCCAAAAGCACCCCCATCTGTCTATCCACTGGCCCTGGAT

Figure 14b

2851 CTGCTGCCAAACTAACTCCATGGTACCCCTGGGATGCCTGGTCAAGGGC
2901 TATTTCCCTGAGCCAGTGACAGTGACCTGGAACCTCTGGATCCCTGTCCAG
2951 CGGTGTGCACACCTTCCCAGCTGTCTGCAGTCTGACCTCTACACTCTGA
3001 GCAGCTCAGTGACTGTCCCCCTCCAGCACCTGGCCAGCGAGACCGTCACC
3051 TGCAACGTTGCCACCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101 GCCCAGGGATTGTACTAGTGGAGGTGAGGTAGCTAAGGGAGATCTCGAC
3151 GGATCCCCGGAAATTGCCCTCTCCCCCTCCCCCCCCCTAACGTTACTGG
3201 CCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTGTCTATATGTTATTT
3251 CCACCATATTGCCGTCTTGGCAATGTGAGGGCCGGAAACCTGGCCCT
3301 GTCTTCTGACGAGCATTCTAGGGTCTTCCCTCTGCCAAAGGAAT
3351 GCAAGGTCTGTGAATGTGAGGAAGCAGTTCTCTGGAAAGCTTCTT
3401 GAAGACAAACAACGTCTGTAGCGACCTTTGCAGGCAGCGGAACCCCCCA
3451 CCTGGCGACAGGTGCCCTCTGCCGGAAAAGCCACGTGTATAAGATACACC
3501 TGCAAAAGGCCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551 AAAAGACTAAATGGCTCTCTCAAGCGTATTCAACAAGGGGCTGAAGGAT
3601 GCCCAGAAGGTACCCATTGTATGGGATCTGATCTGGGGCCTCGGTGAC
3651 ATGCTTACATGTGTTACTCGAGGTAAAAAAACGTCTAGGCCCGGCGA
3701 ACCACGGGACGTGGTTTCTTGGTAAACACGATGATAATATGCCCTC
3751 CTTGTCCTCTGCTCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801 ACATTGTGCTGACACAATCTCAGCAATCATGTCGATCTCCAGGGGAG
3851 AAGGTACCATGACCTGCACTGCAAGCTCAAGTGTAAGTTACATACACTG
3901 GTACCAGCAGAAGTCAGGCCACCTCCCCAAAAGATGGATTATGACACAT
3951 CCAAACGGCTCTGGAGCTCTGCTCGCTTCAGTGGCAGTGGGCTGGG
4001 ACCTCTCACTCTCACACTCAGCAGCATGGAGGTGAAGATGCTGCCAC
4051 TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTGGTGGGGGACCA
4101 AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCA
4151 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCTCAGTCGTTGCTTCTT
4201 GAACAACCTCTACCCAAAGACATCAATGTCAGTGAAGTGGAAAGATTGATGGCA
4251 GTGAAACGACAAAATGGCTCTGAACAGTTGGACTGATCAGGACAGCAA
4301 GACAGCACCTACAGCATGAGCAGCACCCCTACGTTGACCAAGGACGAGTA
4351 TGAACGACATAACAGCTAACCTGTGAGGCCACTCACAAGACATCAACTT
4401 CACCCATTGTCAGAGCTCAACAGGAATGAGTGTAAATAGGGGAGATCT
4451 CGACATCGATAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTG
4501 GTATTCTTAACATATGTTGCTCTTACGCTATGGGATACGCTGTTTA
4551 ATGCCCTTGATCATGCTATTGCTTCCCGTATGGCTTTCATTTCTCTC
4601 CTTGTATAAAATCTGGTGTGCTCTCTTATGGAGGTGTGGCCCGTTG
4651 TCAGGCAACGGCTGGCTGGTGTGCACTGTGTTGCTGACGCAACCCCCACT
4701 GTTGGGGCATTGCCACCCCTGTCAGCTCCCTTCCGGGACTTTCGCTT
4751 CCCCTCCCTATTGCCACGGCGAACTCATGCCGCTGCCCTGCCGCT
4801 GCTGGACAGGGCTGGCTGTTGGCACTGACAAATTCCGTGGTGTGTCG
4851 GGGAAATCATCGTCCTTCCCTGGCTGCTGCCGTGTTGCCACCTGGAT
4901 TCTGCGGGACGTCTCTGCTACGTCCCTTCCGGCCCTCAATCCAGCGG
4951 ACCCTCCCTCCGGCCCTGCTGCCGCTCTGCCCTCTCCGCTCT
5001 CGCCTTCGCCCTCAGACGAGCTGGATCTCCCTTGGCCGCTCCCCGCC
5051 TGATCGATAAAATAAAAGATTATTAGTCTCCAGAAAAAGGGGGGAAT
5101 GAAAGACCCCACCTGTAGGTTGGCAAGCTAGCTAACGCAACCTT
5151 GCAAGGCATGAAAAATACATAACTGAGAATAGAGAAGTTGAGATCAAGG
5201 TCAGGAACAGATGAAACAGCTGAATATGGGCAACAGGATATCTGTGGT
5251 AAGCAGTCCCTGCCCGGCTCAGGGCAAGAACAGATGGAACAGCTGAAT
5301 ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCAGGG
5351 CCAAGAACAGATGGCCCCAGATGCCGTCCAGGCCCTCAGCAGTTCTAGA
5401 GAACCATCAGATGTTCCAGGGTCCCCAAGGGACCTGAAATGACCCCTGT
5451 CCTTATTGAACTAACCAATCAGTTCGCTCTCGCTTCTGTTGCGCGCT
5501 TCTGCTCCCCGAGCTCAATAAAAGAGGCCACACCCCTCACTGGGGCGC
5551 CAGTCCTCCGATTGACTGAGTCGCCGGTACCCGTATCCAATAAAC
5601 CTCTTGCAAGTGCATCCGACTTGTGGTCTCGCTGTTCCCTGGAGGGTCT

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGTCTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

1 GGAATTGCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51 CTTGGAATAAGGCCGGTGTGCGTTGTCTATATGTTATTTCCACCATAT
101 TGCCGTCTTTGGCAATGTGAGGGCCCGAAACCTGGCCCTGTCTTCTG
151 ACGAGCATTCTAGGGGTCTTCCCCTCTGCCAAAGGAATGCAAGGTCT
201 GTTGAATGTCGTGAAGGAAGCAGTTCTCTGGAAGCTTCTGAAAGACAAA
251 CAAAGTCTGTAGCGACCCCTTGCAAGGAGCGGAACCCCCCACCTGGCGAC
301 AGGTGCCTCTGGCCAAAAGCCACGTGTATAAGATAACACCTGCAAAGGC
351 GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCA
401 AATGGCTCTCTCAAGCGTATTCAACAAAGGGCTGAAGGATGCCAGAAG
451 GTACCCCATTGTATGGGATCTGATCTGGGCCTCGGTGCACATGTTAC
501 ATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCCCGAACCACGGGG
551 ACGTGGTTTCTTGGCTGTTGCTTGGCGCCATGGGATATCTAGATC
601 TACCTGTCTTGCGCTGTTGCTTGGCGCCATGGGATATCTAGATC
651 TCGAGCTCGCAAAGCTT

1 - 583 IRES
584 - 628 Modified bovine alpha-S1 casein signal peptide coding region
629 - 668 Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

1 TTTGAAAGACCCCACCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51 TGCAAGGCATGAAAAATACATAACTGAGAATAGAAAAGTTCAAGATCAAG
101 GTCAGGAACAAAGAAACAGCTGAATACCAACAGGATATCTGTGGAAGC
151 GGTCCTGCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGA
201 GGCCAAACAGGATATCTGTGGAAGCAGTCTGCCCTCAGCAGTTCTAGTGA
251 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTCTAGTGA
301 TCATCAGATGTTCCAGGGTCCCCAAGGACCTGAAAATGACCCCTGTACC
351 TTATTTGAACTAACAAATCAGTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401 CGCTCTCCGAGCTCAATAAAAGAGCCACAAACCCCTCACTCGCGCGCA
451 GTCTTCCGATAGACTGCGTCGCCGGTACCCGTATTCCAAATAAGCCT
501 CTTGCTGTTGCATCGAACATGTGGTCTCGCTTCTGGGAGGGTCTC
551 CTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTGGGGGCTCGT
601 CGGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCGGGGAGG
651 TAAGCTGGCCAGCACTTATCTGTCTGTGCGATTGTCTAGTGTCTATG
701 TTTGATGTTATGCGCTGCGTCTGTAAGTGTAGCTAACTAGCTCTGTAT
751 CTGGCAGACCCGCTGGTGGAACTGACGAGTTCTGAAACACCCGGCGCAACC
801 CTGGGAGACCTCCAGGGATTGGGGCCGTTTGTGGCCCGACCTGA
851 GGAAGGGAGTCGATGTGGATTCGACCCCGTCAGGATATGTGGTTCTGG
901 AGGAGACGAGAACCTAAAACAGTTCCCGCTCCGCTGAATTGGCTTT
951 CGGTTTGGAAACCGAAGCCGCGCTTGTCTGCTGAGCGCTGCAGCATC
1001 GTTCTGTGTTGCTCTGTGACTGTGTTCTGTAATTGCTGAAAATTAA
1051 GGGCCAGACTGTTACCACTCCCTTAAGTTGACCTTAGGTCACTGGAAAG
1101 ATGTCGAGCGATCGCTACAACCACTCGGTAGATGTCAGAAAGAGACGT
1151 TGGGTTACCTTCTGCTCTGCAAGATGGCAACCTTAACGTCGGATGGCC
1201 GCGAGACGGCACCTTAACCGAGACCTCATCACCAGGTTAAGATCAAGG
1251 TCTTTCACCTGGCCCGCATGGACACCCAGACCGAGGTCCCTACATCGT
1301 ACCTGGGAAGCCTGGCTTGTGACCCCCCTCCCTGGGTCAGCCCTTTGT
1351 ACACCCCTAACGCCCGCCCTCTCTCCATCCGCCGCTCTCTCCCC
1401 TTGAACCTCTCGTTGCAACCCCGCTCGATCTCCCTTTATCCAGGCC
1451 ACTCCCTCTCTAGGCGCCGAATTCCGATCTGATCAAGAGACAGGATGAG
1501 GATCGTTTCGATGATTGAAACAAGATGGATTGACGCGCAGGTTCTCCGCC
1551 GCTTGGGTTGGAGAGGCTATTGGCTATGACTGGCACAACAGACAATCG
1601 CTGCTCTGATGCCCGTGTTCGGCTGTCAGCCGAGGGGCCGGTT
1651 TTTTGTCAGACGCCACCTGTCGGTGCCTGAATGAACTGCCAGGACGAG
1701 GCAGCGGGCTATCGTGGCTGCCACGACGGGCCGTTCCCTGCGCAGCTGT
1751 GCTCGACGTTGTCAGTAAGCGGGAGGGACTGGCTGATATTGGCGAAG
1801 TGCCGGGGCAGGATCTCTGTCATCTCACCTTGTCTGCCAGAAAGTA
1851 TCCATCATGGCTGATGCAATGCGGGCGCTGCACTACGCTTGTCCGGCTAC
1901 CTGCCCATTCGACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951 GGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAG
2001 GGGCTCGGCCAGCGAAGTGTGCCAGGCTCAAGGCGCCATGCCCGA
2051 CGGCAGGGATCTCGTGTGACCCATGGCGATGCCGCTTGGCAATATCA
2101 TGGTGGAAAATGGCGCTTTCTGGATTCTGATCGACTGTGCCGGCTGGG
2151 GTGGCGGACCGTATCAGGACATAGCGTTGGCTACCGGTGATATTGCTGA
2201 AGAGCTGGCGGCGAATGGGCTGACCGCTCCCTCGTGTGTTACGGTATCG
2251 CGCGCTCCGATTGGCAGGCCATGCCCTCTATGCCCTTGTGACGAGTTC
2301 TTCTGAGCGGGACTCTGGGTTGCAATGACCGACCAAGCGACGCCAAC
2351 CTGCCATCACGAGATTTCGATTCACCCGCCCTCTATGAAAGGTTGGG
2401 CTTCGGAATCGTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGG
2451 ATCTCATGCTGGAGTTCTCGCCACCCGGCTGATCCCTCGCGAGT
2501 TGGTTCACTGCTGCCAGGCTGGACGACCTCGCGGAGTCTACCGGCA
2551 GTGCAAATCCGTCGGCATCCAGGAAACCGAGCAGCGGCTATCCGCGCATCC
2601 ATGCCCGAATGCAAGGAGTGGGGAGGCACGATGGCGCTTGGTCA
2651 GCGGATCCGCCATTGGCATATTGCACTACGTTGATCCATATCATAATATGTAC
2701 ATATTGGCTATTGGCCATTGCACTACGTTGATCCATATCATAATATGTAC
2751 ATTTATATTGGCTCATGTCACATTACCGCCATGTTGACATTGATTATT

Figure 16b

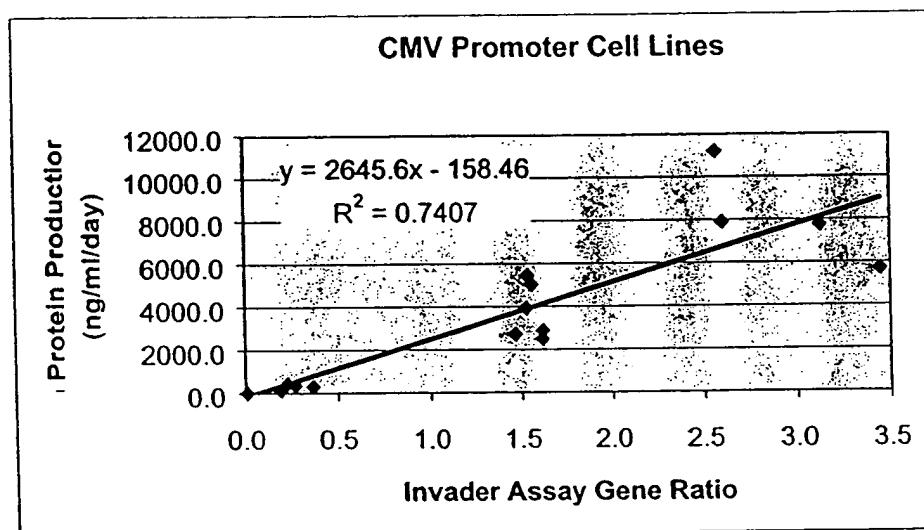
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2851 ATATGGAGTTCCCGTTACATAACTTACGGTAATGGCCCGCTGGCTGA
2901 CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAT
2951 AGTAACGCCAATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTAC
3001 GGTAACACTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
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3101 GTACATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAG
3151 TCATCGCTATTACCATGGTGTGCGGTTTGGCAGTACATCAATGGCGT
3201 GGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCCATGACGT
3251 CAATGGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAATGTC
3301 GTAACAACCTCCGCCCCATTGACGAAATGGCGGTAGGCATGTACGGTGG
3351 GAGGTCTATATAAGCAGAGCTCGTTAGTGAACCGTCAGATCGCTGGAG
3401 ACGCCATCCACGCTGTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451 GCCTCCGGGCCCAAGCTCTCGACGGATCCCGGGATTCAAGGCCATC
3501 GATCCCGCCGCCACCATGGAATGGAGCTGGTCTTCTCTTCTGTGTC
3551 AGTAACATACAGGTGTCACCTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601 CCCTATCTGCATCTGTGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651 GGGAAATTCAAAATTATTAGCATGGTATCAGCAGAAACAGGGAAATC
3701 TCCTCAGCTCTGGCTATAATGCAAAAACCTTACAGCAGATGGTGTGCCAT
3751 CAAGGTTCACTGGCAGTGGATCAGGAACACAATTCTCTCAAGATCAAC
3801 AGCCTGCAGCCTGAAGATTGGGAGTTATTACTGTCAACATTGGAG
3851 TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGAAATCAAACGGGCTG
3901 ATGCTGCACCAACTGTATCCATCTTCCCACCATCAGTGGCAGTTAAC
3951 TCTGGAGGTGCTCACTCCTGTGCTTCTGAACAACACTTCTACCCAAAGA
4001 CATCAATGCAAGTGGAAAGATTGATGGCAGTGAACGACAAAAATGGCGTCC
4051 TGAACAGTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101 AGCACCCCTCACATTGACCAAGGACGGATGATGAACGACATAACAGCTATAAC
4151 CTGTGAGGCCACTCACAAGACATCAACTCACCCATTGTCAGAGCTTCA
4201 ACAGGAATGAGTGTGAAAGCATCGATTCCCTGAATTGCCCTCTCC
4251 CTCCCCCCCCCTAACGTACTGGCGAAGCCGCTTGGATAAGGCCGGT
4301 GTGCGTTGCTATATGTTATTCCACCATATTGCGCTTTGGCAAT
4351 GTGAGGGCCCGAAACCTGGCCCTGCTTCTGACGAGCATTCTAGGGG
4401 TCTTCCCCCTCGCAAAGGAATGCAAGGTCTGTGAATGTCGTGAAGG
4451 AAGCAGTTCTCTGGAGCTTCTTGAAGACAACACAGTCTGTAGCGACC
4501 CTTTGAGGCAGCGAACCCCCCACCTGGCGACAGGTGCTCTGGGCCA
4551 AAAGCCACGTGTATAAGATAACACCTGCAAAGGGGGCACAAACCCAGTGCC
4601 ACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAATGGCTCTCTCAAGC
4651 GTATTCAACAAGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGG
4701 ATCTGATCTGGGCTCGGTGACATGCTTACATGTGTTAGTCGAGGT
4751 TAAAAAAACGCTTAGGCCCCCGAACACGGGGACGTGGTTTCTTGA
4801 AAAACACGATGATAATATGGCTCCTTGTCTCTGCTCTGGTAGGCA
4851 TCCTATTCCATGCCACCCAGGCCAGGTTCACTCAGCAGTCTGGGGCA
4901 GAGCTGTGAAGCCAGGGCCTCACTCAAGTTGTCTGCACAGCTCTGG
4951 CTTCAACATTAAAGACACCTTATGCACTGGGTGAAGCAGAGGCCCTGAAC
5001 AGGGCTGGAGTGGATTGAAAGGATTGATCCTGGAATGGGAAACTGAA
5051 TATGACCGAAGTCCAGGGCAAGGCAACTATAACAGCAGACACATCCCTC
5101 CAAACAGTCACCTGCACTCAGCAGCTGACATCTGAGGACACTGCC
5151 TCTATTACTGTGCTAGTGGAGGGAACTGGGGTTTCTTACTGGGGCAA
5201 GGGACTCTGGTCACTGTCTGCACTGCAACGACACCCCCATCTGTCTA
5251 TCCACTGGCCCTGGATCTGCTGCCAAACTAACTCCATGGTGAACCTGG
5301 GATGCCCTGGTCAAGGGTATTCCTGAGCCAGTGAAGTGAACCTGGAAC
5351 TCTGGATCCCTGTCCAGGGTGTGACACCTTCCAGCTGTCTGCAGTC
5401 TGACCTCTACACTCTGAGCAGCTCACTGACTGTCCCCCTCCAGCACCTGGC
5451 CCAGCGAGACGTCACCTGCAACGTTGCCACCCGGCAGCAGCACCAAG
5501 GTGGACAAGAAAATTGTGCCCCAGGGATTGTACTAGTGGAGGTGGAGGTAG
5551 CCACCATCACCATCACCAATTAACTAGAGTTAAGCAGGCCGTCAGATCTA
5601 GGCCTCCTAGGTGACATCGATAAAATAAAAGATTATTAGTCTCCAG
5651 AAAAAGGGGGAAATGAAAGACCCACCTGTAGGTTGGCAAGCTAGCTTA
5701 AGTAACGCCATTGCAAGGATGGAAAAATACATAACTGAGAATAGAGA
5751 AGTTCAAGATCAAGGTCAAGGAACAGATGGAACAGCTGAATATGGGCAAAC
5801 AGGATATCTGTGGTAAGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGA
5851 TGGAACAGCTGAATATGGGCAAACAGGATATCTGTGGTAAGCAGTTCT

Figure 16c

```
5901 GCCCCGGCTCAGGGCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951 CAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTCCCCAACGGACCT
6001 GAAATGACCGCTGTGCCTTATTGAACCAACCAATCAGTCGCTTCTCGCT
6051 TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101 CTCACTCGGGCGGCCAGTCCTCCGATTGACTGAGTCGCCCGGTACCCGT
6151 GTATCCAATAAACCTCTTGAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201 CCTTGGGAGGGTCTCCTTGAGTGATTGACTACCCGTAGCGGGGGTCTT
TCATT
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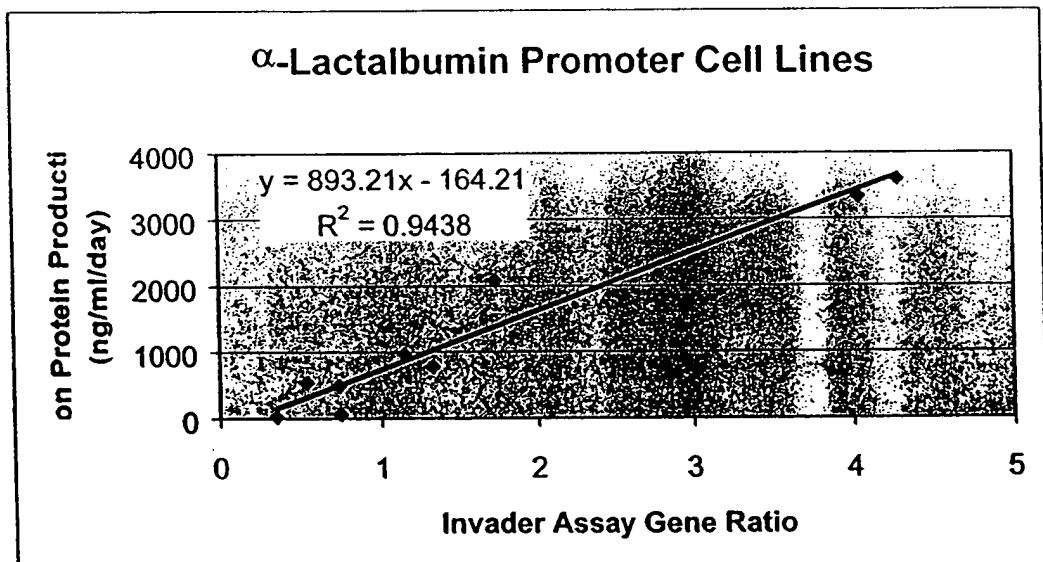
Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α -LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17. CMV construct containing cell lines.



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Figure 18: α -Lactalbumin construct containing cell lines



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Figure 19a
SEQ ID NO: 34
LNBOTDC Vector

1 GAATTAATTCATACCAGATCACCGAAAATGTCTCCAAATGTGTCCCCC
51 TCACACTCCCAAATTGCGGGCTCTGCCTTCTAGACCACTCTACCCCTAT
101 TCCCCACACTCACCGGAGCCAAGGCCGGCCCTCCGTTTCTTGCTTT
151 TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
201 CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAAGATCAAGGT
251 CAGGAACAAAGAACAGCTGAATACCAAACAGGATATCTGTGTAAGCGG
301 TTCTCGCCCGGCTCAGGCCAGAACAGATGAGACAGCTGAGTGTAGGG
351 CAAACAGGATATCTGTGTAAGCAGTCTGCCGGCTCGGGGCAAG
401 AACAGATGGTCCCAGATCGGTCCAGCCCTCAGCAGTTCTAGTGAATC
451 ATCAGATGTTCCAGGTGCCCCAAGGACCTGAAAATGACCTGTACCTT
501 ATTGAACTACCAATCAGTCGCTTCGCTTCTGTCGCGCTTCCG
551 CTCTCGAGCTCAATAAAAGGCCACAACCCCTCACTCGGCCAGT
601 CTTCGATAGACTCGCTGCCGGTACCCGTATCCAAATAAGCCCT
651 TGCTGTTGATCCGAATCGTGGTCTCGCTGTTCTGGGAGGGTCTCT
701 CTGAGTGTGACTACCCACGACGGGGTCTTCTATTGGGGCTCGTCC
751 GGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCACCGGGAGGTA
801 AGCTGGCCAGCAACTTATCTGTGTCGCTGACTAGTTAGCTAACTAGCTGTATCT
851 TGATGTTATGCGCCTGCGTCTGACTAGTTAGCTAACTAGCTGTATCT
901 GGGGGACCCGTGGTGAACGACGGAGTCTGAACACCCGGCCGAACCC
951 GGGAGACGTCCCAGGGACTTGGGGCCGTTTGTGGCCGACCTGAGG
1001 AAGGGAGTCGATGTTGAATCCGACCCCGTCAGGATATGTGGTCTGGTAG
1051 GAGACGAGAACCTAAACAGTTCCCGCCTCCGTCGATTTTGCTTTCG
1101 GTTGGAACCGAAGCCGCGTCTGCTGAGCAGCGCTGAGCATCGT
1151 TCTGTGTTGCTCTGACTGTGTTCTGATTTGTCTGAAAATTAGG
1201 GCCAGACTGTACCACTCCCTAAAGTTGACCTTAGTCAGTGAAAGAT
1251 GTCGAGCGGATCGCTCACACCAGTCGGTAGATGTCAGAAGAGACGTTG
1301 GTTACCTCTGCTCTGAGAATGGCAACCTTAACCTCGGATGGCCGC
1351 GAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAGATCAAGGTC
1401 TTTTACCTGGCCCGCATGGACACCCAGACCCAGGCTCCATCGTGC
1451 CTGGGAAGCCTTGGTTTGACCCCTCCCTGGGCAAGCCCTTTGTAC
1501 ACCCTAAGCCTCCGCTCTCTCCATCCGCCCCGTCCTCCCCCT
1551 GAACTCTCTGTCGACCCCGCCTCGATCCTCCCTTATCCAGCCCTCAC
1601 TCCTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651 AGCTTGTATATCCATTTCGGATCTGATCAGCACGTGTTGACAATTATC
1701 ATCGGCATAGTATATCGGCATAGTATAATACGCAAGGTGAGGAACCTAA
1751 CCATGGCAAGCCTTGTCTCAAGAAGAATCCACCCCTCATTGAAAGAGCA
1801 ACGGCTACAATCACAGCATCCCCATCTGAGAAGACTACAGCGTCGCCAG
1851 CGCAGCTCTCTAGGACGGCGCATCTCACTGGTGTCAATGTATATC
1901 ATTTTACTGGGGACCTTGTGAGAACACTCGTGGTGTGGCACTGCTGCT
1951 GCTGCGGAGCTGGCAACCTGACTTGATCTGTCGCGATCGGAAATGAGAA
2001 CAGGGGCATCTGAGCCCTGCGGACGGTGTGACAGGTGCTCTCGATC
2051 TGCATCTGGGATCAAAGCGATAGTGAAGGACAGTGTGAGACAGCCGACG
2101 GCAGTTGGGATTCTGAAATTGCTGCCCCCTGGTTATGTGTTGGAGGGTA
2151 AGCACTTCGTCGGCAGGGACTGACACGTCGCTACGAGATTTCGAT
2201 TCCACCGCCCTCTATGAAAGGTGGCTTCCGAAATCGTTTCCGGGA
2251 CGCCGGCTGGATGATCTCCAGCGGGGGATCTCATGCTGGAGTTCTCG
2301 CCCACCCAACTTGTATTGCAAGCTATAATGGTTACAAATAAGCAAT
2351 AGCATCACAAATTCAAAATAAGCATTTTCACTGCATTCTAGTTG
2401 TGGTTTGTCAAACCTCATCAATGTATCTTATCATGTCGAGTTGGT
2451 TCAGCTGTCGCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501 AAATCCGTCCGGCATCCAGGAAACCGAGCAGCGCTATCCGCGCATCCATGC
2551 CCCCGAAGTCAGGAGTGGGGAGGCACGATGGCCCTTGGTCAGGGCG
2601 ATCCGGCCATTAGCCATTATTGTCATTGGTTATAGCATAAATCAATAT
2651 TGGCTATTGGCCATTGCACTACGTTGATCCATATCATAATATGTACATT
2701 ATATTGGCTCATGTCCAACATTACGGCCATGTTGACATTGATTATTGACT
2751 AGTTATTAATAGTAATCAATTACGGGTCAATTAGTCATAGCCCATATAT
2801 GGAGTTCCGGTACATAACTTACGGTAATTGGCCCGCTGGCTGACCGC
2851 CCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTA

Figure 19b

2901 ACGCCAATAGGGACTTCCATTGACGTCATGGTGGAGTATTTACGGTA
2951 AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
3001 CTATTGACGTCATGACGGTAAATGGCCCGCTGGCATTATGCCAGTAC
3051 ATGACCTTATGGGACTTCTACTTGGCAGTACATCTACGTATTAGTCAT
3101 CGCTATTACCATGGTATGCCGGTTTGGCAGTACATCAATGGCGTGGAT
3151 AGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAT
3201 GGGAGTTTGGTGGCACCRAAATCAACGGGACTTCCAATGTCGTA
3251 CAACTCCGCCCATGACGCAAATGGCGGTAGGCATGTACGGTGGGAGG
3301 TCTATATAAGCAGAGCTGTTAGTGAACCGTCAGATGCCCTGGAGACGC
3351 CATCCACGCTGTTTGACCTCCATAGAAGACACGGGACCGATCCAGCCT
3401 CCGCGGCCCAAGCTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451 TTCCCGACTGAAAAGCGGGCAGTGGACGCAACGCAATTATGTGAGTTAG
3501 CTCACTCATTAGGCACCCCAGGCTTACACTTTATGCTTCCGGCTCGTAT
3551 GTTGTGTGAAATTGTGAGCGGATAACAATTACACAGGAAACAGCTATG
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3651 GCCGCCAGTGTGCTGGAATTCAACCATGGGCAACCCGGGAAACGGCAGCGC
3701 CTTCTGCTGGCACCCATGGAAAGCCATGCCGGGACACGACGTCACGC
3751 AGCAAAGGGACGAGGTGTGGTGGCATGGGATCGTCATGTCATCTC
3801 ATCGTCTGGCCATCGTGTGGCAATGTGCTGGTCATCACAGCATTG
3851 CAAGTCGAGCGCTGCAGACGGTCACCAACTACTTCATCACAAGCTTG
3901 CCTGTGCTGATCTGGTCATGGGCTAGCAGTGGTGCCTTGGGCC
3951 CATATTCTCATGAAAATGTGGACTTTGGCAACTTCTGGTGGAGTTCTG
4001 GACTTCATTGATGTGCTGCGTCACGGCATCGATTGAGACCCGTGCG
4051 TGATCGCAGTCGACCGCTTGGCATTACTAGTCCTTCAAGTACCAAG
4101 AGCCTGCTGACCAAGAATAAGGCCGGTGTGATCATTCTGATGGTGTGGAT
4151 TGTGTCAGGCCCTACCTCCTTGCCTCAGATGCACTGGTACAGGG
4201 CCACCCACCAAGGAAGCCATCAACTGCTATGCCATTGCTGTGAC
4251 TTCTTCACGAACCAAGCTATGCCATTGCTCTTCCATCGTGTGCTTCTA
4301 CGTCCCCCTGGTATGGTCTTCGTTACTCCAGGGCTTTCAGGAGG
4351 CCAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTC
4401 CAGAACCTTGAAGGTGGAGCAGGATGGGGGACGGGGCATGGACTCCG
4451 CAGATCTTCAAGTCTGTTGAAGGGACCAAAGCCCTCAAGACGTTAG
4501 GCATCATCATGGGCACTTCAACCTCTGCTGGCTGCCCTTCTCATCGTT
4551 AACATTGTGATGTGATCAGGATAACCTCATCCGTAAAGGAAGTTACAT
4601 CCTCTTAAATTGGATAGGCTATGTCATTCTGGTTCAATCCCTTATCT
4651 ACTGCCGGAGCCCAGATTTCAGGATTGCCATTGCTACTCCAGCAACGGAA
4701 CGCAGGTCTCTTGAGGCCTATGCCATTGCTACTCCAGCAACGGAA
4751 CACAGGGGAGCAGAGTGGATATCACGTGAAACAGGGAGAAGAAAATAAAC
4801 TGCTGTGAGAGCCTCCAGGACCGGAAGACTTGTGGGCCATCAAGGT
4851 ACTGTGCTTAGCGATAACATTGATTCAACAGGGAGGATTGTAAGTACAAA
4901 TGAACACTGCTCTCGAGAATCGAGGGCGGGCACCACCATCATCACCACG
4951 TCGACCCCGGGACTACAAGGATGACGATGACAAGTAAGCTTATCCATC
5001 ACACGGCCGCGCTCGAGCATGCTAGCGGGCGCTCGAGGGCGGCAA
5051 GGGCGGATCCCCGGAAATTGCCCTCTCCCTCCCCCCCCCTAACGTTA
5101 CTGGCCGAAGCCGCTTGAATAAGGCCGGTGTGCGTTGTCTATATGTAA
5151 TTTCCACCATATTGCCCTTGGCAATGTGAGGGGGGGAAACCTGG
5201 CCTGTCCTTGAAGGAGATTCTAGGGTCTTGGGCTCTGCCAAAG
5251 GAATGCAAGGCTCTGGATGTGTCAGGAAAGCAGTCTCTGGAAGCT
5301 TCTTGAAGACAAACAAAGCTGTAGCGACCCCTTGCAGGCAAGCGGAACCC
5351 CCCACCTGGCGACAGGTGCCTGCCGGCAAAGGCCAGTGTATAAGATA
5401 CACCTGCAAAGGGCACAACCCAGTGCACGGTGTGAGTTGGATAGTT
5451 GTGAAAGAGTCAAATGGCTCTCTCAAGCGTATTCAACAAGGGCTGAA
5501 GGATGCCCAAGAAGGTACCCATTGTATGGGATCTGATCTGGGCCCTCGGT
5551 GCACATGCTTACATGTGTTAGTCAGGTTAAACAGTCTAGGCC
5601 CGAACACCAGGGGACGTGGTTTCTTGAAGGAAACACGATGATAATATGG
5651 CCTCTTGTCTCTGCTCTGGTAGGCATCTTATCCATGCCACCCAG
5701 GCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGCTCTGGCGAGAG
5751 GGCCACCATCAACTGCAAGTCCAGCCAGGTGTTGTACAGCTCCAACA
5801 ATAAGAACTATTAGCTGGTATCAGCAGAAACAGGACAGCCTCTAAG
5851 CTGCTCATTACTGGCATCTACCCGGAAATCCGGGGCTGACCGATT
5901 CAGTGGCAGGGCTGGCAGAGATTCACTCTCACCATCAGCAGCTGC
5951 AGGCTGAAGATGTGGCAGTTATTACTGTCAGCAATATTAGTACTCAG

Figure 19c

6001 ACGTTCGGCCAAGGGACCAAGGTGAAATCAAACGAACGTGGCTGCACC
6051 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACGTG
6101 CCTCTGTTGTGCTGCTGTAATAACTCTATCCAGAGAGGCCAAAGTA
6151 CAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGA
6251 CGCTGAGCAAAGCAGACTACGAGAAAACAAAACCTACGGCTCCGGAAGTC
6301 ACCCATCAGGGCCTGAGATGCCCGTCACAAAGAGCTTCACAAAGGGGAG
6351 AGTGTAGTTCTAGATAATTAAATTAGGAGGAGATCTGAGCTCGCGAAAG
6401 CTTGGCACTGGCGTCGTTTACAACGTCGTGACTGGGAAACCCCTGGCG
6451 TTACCCAACCTTAATCGCCTGCAAGCACATCCCCCTTCGCCAGCCTCTA
6501 GGTGACATCGATAAAAATAAAAGATTATTTAGTCTCCAGAAAAGGGG
6551 GGAATGAAAGACCCCACCTGTTAGGTTGGCAAGCTAGCTTAAGTAACGCC
6601 ATTTGCAAGGCATGGAAAAAATACATAACTGAGAATAGAGAAAGTTCAAG
6651 CAAGGTAGGGACAGATGGAACAGCTGAATATGGGCAAACAGGATATCT
6701 GTGTTAAGCAGTTCTGCCCGGTCAGGGGCAAAGAACAGATGGAACAGC
6751 TGAATATGGGCAAACAGGATATCTGTTAAGCAGTTCTGCCCGGCT
6801 CAGGGCAAGAACAGATGGTCCCAGATGCCGTCAGGGGCTCAGCAGTT
6851 CTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGACC
6901 CTGTCCTTATTGAACTAACCAATCAGTCGCTCTCGCTTCTGTTCGC
6951 GCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCACAACCCCTACTCGG
7001 GGCCTTCACTGGCTGCTCGCGCTTCGGTGTAGCAGGTTCTGGGAG
7051 AAACCCCTTTCGACTTGCATCCGACTTGTGTTCTCGCTGTTCTGGGAG
7101 GGTCTCTCTGAGTGATTGACTACCCGTCAAGCGGGGTCTTCAATTGGG
7151 GGCTCGTCCGGGATCGGGAGACCCCTGCCAGGGACCACGCCACAC
7201 CGGGAGGTAAGCTGGCTGCCCGCGTTTCGGTGTAGCAGGGTAAAACC
7251 TCTGACACATGCAGCTCCGGAGACGGTCACAGCTGTCTGTAAGCGGAT
7301 GCCGGGAGCAGACAAGCCGTCAAGGCCGTCAGGGCGTCAGCGGGGTGTTGGCGGGTG
7351 TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401 GCTTAACATAGCGGCATCAGAGCAGATTGACTGAGAGTGCACCATATGC
7451 GGTGTGAAATACCGCACAGATGCGTAAGGGAGAAAATACCGCATCAGGCG
7501 TCTTCGGCTTCTCGCTACTGACTCGCTCGCTCGGTCTCGCTGCG
7551 GCGAGCGGTATCAGCTACTCAAAGCGGTAAATACGGTTATCCACAGAAAT
7601 CAGGGGATAACCGAGGAAAGAACATGTGAGCAAAGGCCAGCAAAGGCC
7651 AGGAACCGTAAAAGGCCGCGTTGCTGGCTTTCCATAGGCTCCGCC
7701 CCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCAAACCC
7751 CGACAGGACTATAAGATACCAGCGTTTCCCGTGGAAAGCTCCCTCGT
7801 CGCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTGTCGCCCTTCT
7851 CCCTCGGGAAAGCGTGGCGTTCTCATAGCTCACGCTGTAGGTATCTCA
7901 GTCCGGTGTAGGTGCTCGCTCAAGCTGGCTGTGCAACGACCCCC
7951 GTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTGAGTCAA
8001 CCCGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGA
8051 TTAGCAGAGCGAGGTATGTAAGCGGTGCTACAGAGTTCTGAGTGGGG
8101 CCTAACTACGGCTACACTAGAAGGCAGTATTGGTATCTGCGCTCTGCT
8151 GAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTGATCCGGCAAAC
8201 AAACCCCGCTGGTAGCGGTGGTTTTTTGTTGCAAGCAGCAGATTACG
8251 CGCAGAAAAAAAGGATCTCAAGAAGATCCCTTGATCTTCTACGGGTC
8301 TGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTGGTATGAGAT
8351 TATCAAAAAGGATCTCACCTAGATCTTTAAATTAAAAATGAAGTTT
8401 AAATCAATCTAAAGTATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451 CTTAATCAGTGAGGCACCTATCTCAGCGATCTGCTATTCGTTCATCA
8501 TAGTTGCTGACTCCCGCTGTTAGATAACTACGATACGGGAGGGCTTA
8551 CCATCTGGCCCCAGTGTGCAATGATACCGCAGACCCACGCTCAGGG
8601 TCCAGATTATCAGCAATAAAACCGCCAGCCGAAGGGCGAGCGCAGAA
8651 GTGGTCTGCAACTTTATCCGCCCTCATCCAGTCTATTAAATTGTCGG
8701 GAAGCTAGAGTAAGTAGTGTGCTTAATAGTTGCGCAACGTTGTC
8751 CATTGCTGCAGGCATGTGGTGTCACTGCTCGTGTGGTATGGCTTCAT
8801 TCAGCTCCGGTTCCCAACGATCAAGGCAGTTACATGATCCCCCATGTTG
8851 TGCAAAAAGCGGTTAGCTCTCGGTCTCCGATCGTTGTCAGAAAGTAA
8901 GTTGGCCGAGTGTATCACTCATGGTTATGGCAGCAGTGTGACTTC
8951 TTACTGTCATGCCATCCGTAAGATGCTTTCTGACTGTTGAGTACTCA
9001 ACCAAGTCATTCTGAGAATAGTGTATGCCGACCCAGTTGCTCTGCC
9051 GGCCTCAACACGGATAATACCGGCCACATAGCAGAACTTTAAAAGTGC

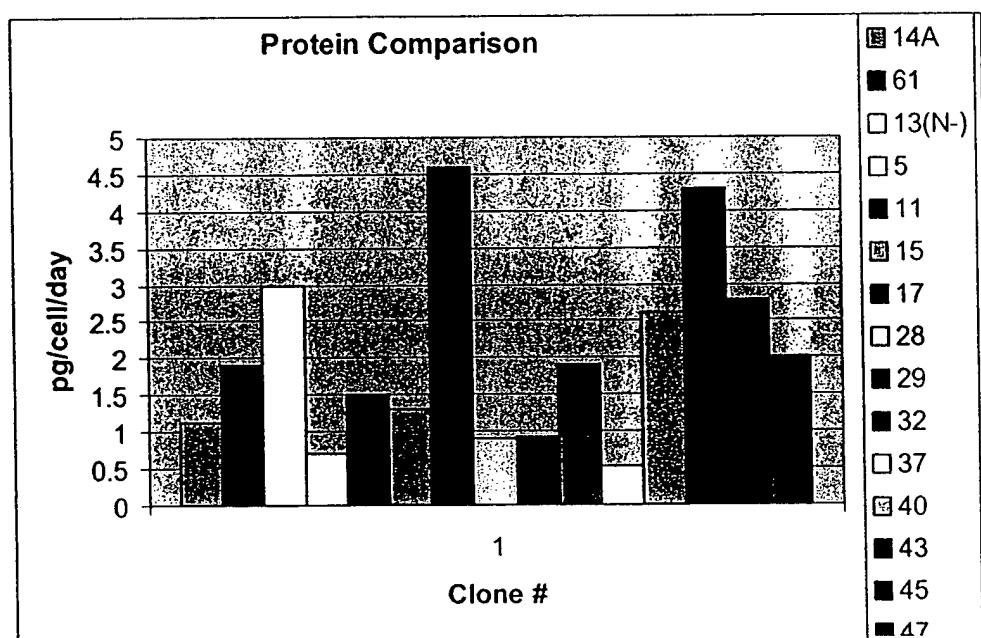
Figure 19d

9101 TCATCATTGGAAAACGTTCTCGGGCGAAAACCTCTCAAGGATCTTACCG
9151 CTGTTGAGATCCAGTCGATGTAACCCACTCGTCACCCAACTGATCTTC
9201 AGCATCTTTACTTCACCAGCGTTCTGGGTGAGCAAAAACAGGAAGGC
9251 AAAATGCCGCAAAAAGGGAATAAGGGCAGACCGAAATGTTGAATACTC
9301 ATACTCTTCTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCT
9351 CATGAGCGGATACATATTGAATGTATTAGAAAAATAACAAATAGGGG
9401 TTCCGCGCACATTCGGGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451 ATTATCATGACATTAACCTATAAAAATAGGCGTATCAGGAGGCCCTTCG
1. TCTTCAAGAAT

Features:

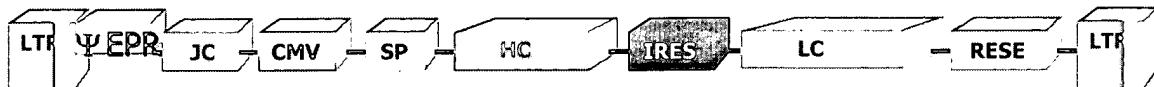
149-737 Moloney murine sarcoma virus 5' LTR
807-1616 Extended Packaging Region
1680-1735 EM7 promoter (bacteriophage T7 promoter)
1754-2151 Blasticidin resistance gene coding sequence
2310-2440 SV40 poly A signal and site
2603-3420 CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646 IRES
5647-5703 Bovine α -lactalbumin signal peptide
5704-6372 'humanized' antibody light chain
6553-7146 MoMuLV 3' LTR
7683Origin of replication
9302-8442 β -Lactmase coding sequence

Figure 20



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Figure 21(A). Gene Sequence of a Single Retrovector IgM Construct (SEQ ID NO:37)



LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
 Psi EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
 JC = J Chain Gene
 CMV = Simian Cytomegalovirus Promoter Region
 SP = Heavy Chain Signal Peptide
 HC = Mu Heavy Chain Gene
 IRES = Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
 LC = Kappa or Lambda Light Chain Gene
 RESE = RNA Export and Stability Element
 LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGTCATTAGTTCAT
 AGCCCATATATGGAGTTCCCGCGTTACATAACTACGGTAAATGGCCCGCTGGCTGACC
 GCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
 TAGGGACTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTGGCA
 GTACATCAAGTGTATCATATGCCAAGTACGCCCCATTGACGTCAATGACGGTAAATG
 GCCCGCCTGGCATTATGCCAGTACATGACCTATGGGACTTCTACTTGGCAGTACA
 TCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTGGCAGTACATCAATGGG
 CGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
 GAGTTGTTTGGCACCAAAATCAACGGACTTCCAAAATGTCGTAACAACCTCCGCC
 CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTAA
 TAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTGCGTCGCCCG
 GGTACCCGTATTCCAATAAGCCTCTTGTGTTGCATCCGAATCGTGGCTCGCTGT
 TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTTGGG
 GGCTCGTCCGGGATTGGAGACCCCTGCCAGGGACCCACCGACCGGGAGGTA
 AGCTGGCCAGCAACTTATCTGTGCTGTCGATTGTCTAGTGTCTATGTTGATGTTAT
 GCGCCTCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGAA
 CTGACGAGTTCTGAACACCCGGCCGAACCTGGGAGACGTCCCAGGGACTTGGGGC
 CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTCAGGATA
 TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCTCCGTCTGAATTTC
 TTTCGGTTTGGAACCGAAGCCGCGCTCTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
 TGTTGTCTCTGTGACTGTGTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTAC
 CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACACC
 AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACC
 TTTAACGTCGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA
 GATCAAGGTCTTTCACCTGGCCCGATGGACACCCAGACCCAGGTCCCTACATCGTGA
 CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCCTAAG
 CCTCCGCCTCCTCTCCATCCGCCCCGTCTCTCCCCCTGAACCTCCTCGTTGAC

FIGURE 21 (B)

CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGAATTCCGA
TCTGATCAAGAGACAGGATGAGAAGTCAAGATGAAGAACCATTGCTTTCTGGGGAGT
CCTGGCGGTTTTATTAAGGCTGTTCATGTGAAAGCCAAAGAAGATGAAAGGATTGTT
TTGTTGACAACAAATGTAAGTGTGCCGGATTACTCCAGGATCATCGTCTTCCGAA
GATCCTAATGAGGACATTGTGGAGAGAAACATCCGAATTATTGTTCTCTGAACAAACAG
GGAGAATATCTCTGATCCCACCTCACCATTGAGAACAGAGATTGTGTACCATTTGTCTG
ACCTCTGTAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCT
ACCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAG
AAACAAGTGTACACAGCTGGTCCCACCGTATATGGTGGTGGACCAAAATGGTGG
AAACAGCCTAACCCAGATGCCGCTATCCTGACTAAAGATCCCTATGGCTATTGGCCA
GGTCAATACTATGTATTGCCCTATGCCATATAGTATTCCATATATGGGTTTCCTAT
TGACGTAGATGCCCTCCAATGGCGGTCCCATATACCATATATGGTCTTCCTAAT
ACCGCCCATAGCCACTCCCCATTGACGTCATGGTCTATATATGGTCTTCCTAATT
GACGTCATATGGCGGTCTATTGACGTATATGGCGCTCCCCATTGACGTCATTAC
GGTAAATGGCCCGCTGGCTCAATGCCATTGACGTCATAGGACCACCCACCATGAC
GTCAATGGATGGCTCATGCCATTGACGTACATCAATATCTATTAAATAGTAACGGCAAGT
TGACGGTAAATGGCCCACGGCAGTACATCAATATCTATTAAATAGTAACGGCAAGT
ACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCATGGC
GGTAAATGGCCCGCATGGCTGCCAGTACATCCCCATTGACGTCATGGGAGGGCA
ATGACGCAAATGGCGTCCATTGACGTAATGGCGGTAGGCGTGCCTAATGGGAGGT
CTATATAAGCAATGCTGTTAGGGAACCGCCATTGCGCTGGGACGTCGGAGGAGCT
CGAAAGCTTAGGACCTCACCATGGATGGAGCTGTATCATCCTCTTGGTAGCAACA
GCTACAGGTGTCACCCGAGGTCCAACGGTGGAGAGCGGTGGAGGGTGTGCAACC
TGGCCGGTCCCTGCGCCTGCTCGCATCTGGCTTCGATTTCACCATATTGGA
TGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGATTGGAGAAATTCA
GATAGCAGTACGATTAACATGCGCGTCTCTAAAGGATAGATTACAATATCGCGAGA
CAACGCCAAGAACACATTGTTCTGCAAATGGACAGCCTGAGACCCGAAGACACCGGG
TCTATTTTGCAAGCCTTACTCGGCTCCCTGGTTGCTTATTGGGCCAAGGG
ACCCCGGTACCGTCTCCTCAGGGAGTGCATCGCCCCAACCTTCCCTCGTCTC
CTGTGAGAATTCCCGTCGGATACGAGCAGCGTGGCGTTGGCTGCCTCGCACAGGACT
TCCTTCCGACTCCATCACTTGTCCGGAAATACAAGAACAACTCTGACATCAGCAGT
ACCCGGGCTCCCATCAGTCCGAGAGGGGAAGTACGCGACCCACCTCACAGGTGCT
GCTGCCCTCAAGGACGTATGCAGGGCACAGACGAACACGTGGTGTGCAAAGTCCAGC
ACCCCAACGGCAACAAAGAAAAGAACGTGCCCTTCCAGTGATTGCCAGCTGCCCTCC
AAAGTGAGCGTCTCGTCCACCCCGCAGGGCTTCTCGCAACCCCGCAAGTCCAA
GCTCATCTGCCAGGCCACGGTTTCAGTCCCGGCAGATTAGGTGTGCTGGCG
AGGGGAAGCAGGTGGGTCTGGCGTACCCACGGACCAGGTGCAGGCTGAGGCCAAGAG
TCTGGGCCACGACCTACAAGGTGACCAGCACACTGACCATCAAAGAGAGCGACTGGCT
CGGCCAGAGCATGTTCACCTGCCCGTGGATCACAGGGCCTGACCTCCAGCAGAATG
CGTCCTCCATGTGTCCCCGATCAAGACACAGCCATCCGGTCTCGCCATCCCCCA
TCCTTGCCAGCATCTCCTCACCAAGTCCACCAAGTTGACCTGCCCTGGTCACAGACCT
GACCACCTATGACAGCGTACCGATCTCCGACCCGCAGAATGGCGAAGCTGTGAAA
CCCACACCAACATCTCCGAGAGCCACCCCAATGCCACTTCAGCGCCGTGGGTGAGGCC
AGCATCTGCGAGGATGACTGGAATTCCGGGAGAGGTTACGTGCACCGTGACCCACAC

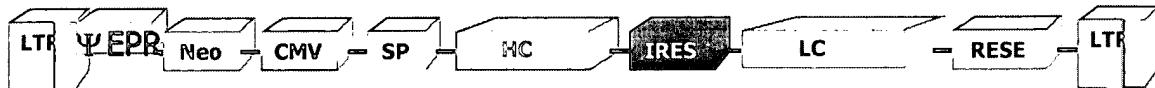
FIGURE 21 (C)

AGACCTGCCCTGCCACTGAAGCAGACCATCTCCGGCCAAGGGGGTGGCCCTGCACA
GGCCCGATGTCTACTTGCTGCCACCAGCCGGAGCAGCTGAACCTGCAGGGAGTCGGCC
ACCATCACGTGCCCTGGTACGGGCTCTCTCCCGCGACGCTTCGTGCAGTGGATGCA
GAGGGGGCAGCCCTGTCCCCGGAGAAGTATGTGACCAGCGCCCAATGCCTGAGCCCC
AGGCCCCAGGCCGGTACTTCGCCACAGCATCCTGACC GTGCCAGAGGAATGGAAC
ACGGGGGAGACCTACACCTGCGTGGCCATGAGGCCCTGCCAACAGGGTCACCGAGAG
GACCGTGGACAAGTCCACCGGTAAACCCACCCGTACAACGTGTCCCTGGTCATGTCCG
ACACAGCTGGCACCTGCTACTGAGATCTCTGCAGAAACGGCCTAGGTTGGAAATT
GCCCTCTCCCTCCCCCCCCCTAACGTTACTGGCCAAGCCGCTTGAATAAGGCCGGT
GTGCGTTGTCTATATGTTATTTCCACCATATTGCCGTCTTGGCAATGTGAGGGCC
CGGAAACCTGGCCCTGTTCTTGACGAGCATTCTAGGGTCTTCCCTCGCCAA
AGGAATGCAAGGTCTGTGAATGCGAAGGAAGCAGTCCCTCTGGAAGCTCTTGAA
GACAAACAACGTCTGTAGCGACCCTTGACGGCAGCGGAACCCCCCACCTGGCGACAGG
TGCCTCTGCCGAAAGCCACGTGTATAAGATAACACCTGCAAAGGCCGACAACCCCA
GTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAGTCAAATGGCTCTCAAGCGTAT
TCAACAAGGGCTGAAGGATGCCAGAAGGTACCCATTGTATGGATCTGATCTGGGG
CCTCGGTGCACATGTTACATGTGTTAGTCGAGGTTAAAAAAACGTCTAGGCC
GAACCAACGGGACGTGGTTTCTTGAACACAGATGATAATATGGCCTCTTGTC
TCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCCAGCTGACCCA
GAGCCAAGCAGCCTGAGGCCAGCGTGGTGACAGAGTGACCATCACCTGTAAGGCC
GTCAGGATGTGGTACTCTGTAGCCTGGTACCAAGCAGAAGCCAGGTAAAGGCTCAAAG
CTGCTGATCTACTGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTAGCGGTAG
CGGTAGCGGTACCGACTCACCTCACCACAGCAGCCTCCAGCCAGAGGACATGCCA
CCTACTACTGCCAGCAATATAGCCTCTATCGGTGTTGCCAAGGGACCAAGGTGGAA
ATCAAACGAACTGTGGCTGCACCATCTGCTTCACTTCCGCCATCTGATGAGCAGTT
GAAATCTGGAACTGCCTCTGTTGTGCTGAATAACTCTATCCAGAGAGGCCA
AAGTACAGTGGAAAGGTGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGTACA
GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCGTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCCTGCAAGTCACCCATCAGGGCCTGAGCTCGC
CCGTCACAAAGAGCTTCAACAGGGAGAGTGTAGATCTGTTAACCTAGGCTCGAGTT
CGACATCGATAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTGGTATTCTTA
ACTATGTTGCTCCTTACGCTATGTGGATACGCTGCTTAATGCCCTTGATCATGCT
ATTGCTTCCCGTATGGCTTCACTTCTCCTTGTATAAATCCTGGTTGCTGTCTCT
TTATGAGGAGTTGTGGCCGTTGTCAGGCAACGTGGCGTGGTGTGCAGTGTGTTGCTG
ACGCAACCCCCACTGGTGGGCATTGCCACCCACCTGTCAAGCTCCTTCCGGACTTTC
GCTTCCCGTCCCTATTGCCACGGCGGAACTCATGCCGCCTGCCCTGCCGCTGCTG
GACAGGGCTGGCTGTTGGCACTGACAATTCCGTGGTGTGCGGGAAATCATCGT
CCTTCCCTGGCTGCTGCCCTGTGTTGCCACCTGGATTCTGCGCGGACGTCCCTCTGC
TACGTCCCTCGGCCCTCAATCCAGCGGACCTCCTCCCGGCCCTGCTGCCGCTCT
GCCGCCTCTCCGCGTCTGCCCTCAGACGAGTCGGATCTCCCTTGGCC
CCTCCCGCATCGATAAAATAAAAGATTATTTAGTCTCCAGAAAAAGGGGGAAATGA
AAGACCCCACCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGG
AAAAATACATAACTGAGAATAGAGAAGTTAGATCAAGGTCAAGGAACAGATGGAACAGC
TGAATATGGCCAAACAGGATATCTGTGGTAAGCAGTCAGTCCCTGCCCGCTCAGGGCCAA

FIGURE 21 (D)

GAACAGATGGAACAGCTGAATATGGGCCAACAGGATATCTGTGGTAAGCAGTTCCCTGC
CCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATCGGGTCCAGCCCTCAGCAGTTCT
AGAGAACCATCAGATGTTCCAGGGTCCCCAAGGACCTGAAATGACCCTGTGCCTTAT
TTGAACTAACCAATCAGTCGCTTCTCGCTTCTGTCGCGCGCTTCTGCTCCCCGAGCT
CAATAAAAGAGCCCACAACCCCTCACTCGGGCGCCAGTCCTCCGATTGACTGAGTCGC
CCGGGTACCCGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCT
GTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTAGCGGGGTCTTCATT

Figure 22(A). Gene Sequence of a Double Retrovector IgM Heavy and Light Chain Construct (SEQ ID NO:38).



LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
Neo =	Neomycin Resistance Gene
CMV =	Simian Cytomegalovirus Promoter Region
SP =	Heavy Chain Signal Peptide
HC =	Mu Heavy Chain Gene
IRES =	Internal Ribosome Entry Site/α-Lactalbumin Signal Peptide
LC =	Kappa or Lambda Light Chain Gene
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAAATAGTAATCAATTACGGGGTCAATTAGTTCAT
 AGCCCATATATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
 GCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
 TAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCA
 GTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGTAAATG
 GCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTACTTGGCAGTACA
 TCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGG
 CGTGGATAGCGGTTTGAUTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
 GAGTTGTTTGGCACCAAAATCAACGGACTTCCAAAATGTCGAACAACCTCGGCC
 CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
 TAAAAGAGCCCACAACCCCTCACTCGCGCGCAGTCTCCGATAGACTGCGTCGCCCG
 GGTACCGTATTCCAATAAAGCCTTGTGCTTGCATCCGAATCGTGGCTCGCTGT
 TCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTTGGG
 GGCTCGTCCGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCGGGAGGTA
 AGCTGGCCAGCAACTTATCTGTCTGTCCGATTGTCTAGTGTCTATGTTGATGTTAT
 GCGCCTGCGTCTGTACTAGTTAGCTAAGTCTGTATCTGGCGGACCCGTGGTGGAA
 CTGACGAGTTCTGAACACCCGGCGCAACCTGGGAGACGTCCCAGGGACTTGGGGC
 CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
 TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCGTCTGAATTGG
 TTTCGGTTGGAACCGAAGCCGCGCGTCTGTCTGCTGCAGCGCTGCAGCATCGTTCTG
 TGTTGTCTGTGACTGTGTTCTGTATTGTCTGAAAATTAGGCCAGACTGTTAC
 CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTACAACC
 AGTCGGTAGATGTCAAGAACGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGCCAAC
 TTTAACGTCGGATGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA

FIGURE 22 (B)

GATCAAGGTTTTACCTGGCCCGATGGACACCCAGACACCAGGTCCCCTACATCGTGA
CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCTAAG
CCTCCGCCTCCTCTCCATCGCCCCGTCTCTCCCCCTGAACCTCCTCGTTGAC
CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGGAATTCCGA
TCTGATCAAGAGACAGGATGAGGATCGTTCGATGATTGAACAAGATGGATTGCACGC
AGGTTCTCCGGCGCTGGGTGGAGAGGCTATTGGCTATGACTGGCACAACAGACAA
TCGGCTGCTCTGATGCCCGTGTCCGGCTGTCAGCGCAGGGCGCCGGTTCTTTT
GTCAAGACCGACCTGTCCGGTGCCTGAATGAACACTGCAGGACGAGGAGCGCG
GTGGCTGGCCACGACGGCGTCTTGCAGCTGTGCTCGACGTTGCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGCGAAGTGCCGGGCAGGATCTCCTGTCATCTCACCT
GCTCCTGCCAGAGAAAGTATCCATCATGGCTGATGCAATGCCGGCTGCATACGCTTGA
TCCGGCTACCTGCCCATCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
GGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGCTCGC
CCAGCCGAACTGTTGCCAGGCTCAAGGCCGCATGCCGACGGCGAGGATCTGTCGT
GACCCATGGCGATGCCCTGCTTGCAGAATATCATGGTGGAAAATGCCGCTTCTGGAT
TCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACC
CGTGTATTGCTGAAGAGCTTGGCGCGAATGGGCTGACCGCTCTCGTGTCTTACGG
TATGCCGCTCCGATTGCAAGCCGCATGCCCTCTATGCCCTTGTGACGAGTTCTTCT
GAGGATCCCTATGGCTATTGCCAGGTTCAATACTATGTATTGCCCTATGCCATATAG
TATTCCATATATGGGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCCCT
ATACCATATATGGGCTTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGG
TCTCTATATATGGTCTTCCTATTGACGTATATGGCGGTCTATTGACGTATATGGC
GCCTCCCCATTGACGTCAATTACGGTAATGCCCGCTGGCTCAATGCCATTGACG
TCAATAGGACCACCCACCATTGACGTCAATGGGATGGCTATTGCCATTCAATCCGT
TCTCACGCCCTATTGACGTCAATGACGGTAATGCCCGCTGGAGTACATCAATA
TCTATTAATAGTAACCTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGC
AGTACTCCCATTGACGTCAATGGCGGTAAATGCCCGCGATGGCTGCCAAGTACATCCC
CATTGACGTCAATGGGAGGGCAATGACGCAAATGGCGTTCCATTGACGTAAATGGG
CGGTAGGCGTGCCTAATGGAGGTCTATATAAGCAATGCTCGTTAGGAACCGCCATT
CTGCCTGGGACGTCGGAGGAGCTCGAAAGCTTAGGACCTACCATGGGATGGAGCTGT
ATCATCCTCTTGTAGCAACAGCTACAGGTGTCCTCCGAGGTCCAATGGTGG
GAGCGGTGGAGGTGTTGCAACCTGCCCGTCCCTGCGCCTGCTCCGATCTG
GCTTCGATTCACCACATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTT
GAGTGGATTGGAGAAATTCACTCCAGATAGCAGTACGATTAACATGCGCCGTCTCTAA
GGATAGATTACAATATCGCGAGACAACGCCAAGAACACACATTGTTCTGCAAATGGACA
GCCTGAGACCCGAAGACACCGGGTCTATTGTGCAAGCCTTACTCGGCTTCCCC
TGGTTGCTTATTGGGCAAGGGACCCGGTACCGTCTCTCAGGGAGTGACATCCGC
CCCAACCCCTTCCCCCTCGTCTCTGTGAGAATTCCCCGTGGATACGAGCAGCGTGG
CCGTTGGCTGCCCTCGCACAGGACTCCCTCCGACTCCATCACTTGTCTGAAATAC
AAGAACAACTCTGACATCAGCAGTACCCGGCTTCCCATCAGTCCTGAGAGGGGCAA
GTACGAGCCACCTCACAGGTGCTGCTGCCCTCAAGGACGTATGCAGGGCACAGACG
AACACGTGGTGTGCAAAGTCCAGCACCCAAACGGCAACAAAGAAAAGAACGTGCTT
CCAGTGATTGCCAGCTGCCCTCCAAAGTGAGCGTCTCGTCCCACCCCGCACGGCTT
CTCGCAACCCCGCAAGTCAAGCTCATGCCAGGCCACGGTTCAAGTCCCCGGC

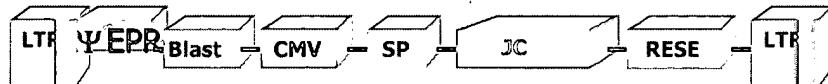
FIGURE 22 (C)

AGATTCAAGGTGCTGGCTGCGCGAGGGGAAGCAGGTGGGTCTGGCGTCACCACGGAC
CAGGTGCAGGCTGAGGCCAAAGAGTCTGGGCCACGACCTACAAGGTGACCAGCACACT
GACCATCAAAGAGAGCGACTGGCTGGCCAGAGCATGTTCACCTGCCCGTGGATCACA
GGGGCCTGACCTTCCAGCAGAATGCGTCCTCCATGTGTGCCCCGATCAAGACACAGCC
ATCCGGGTCTCGCCATCCCCCATCCTTGCAGCATCTCCTCACCAAGTCCACCAA
GTTGACCTGCCTGGTCACAGACCTGACCGACCTATGACAGCGTGACCATCTCCTGGACCC
GCCAGAAATGGCGAAGCTGTGAAAACCCACACCAACATCTCCGAGAGGCCACCCCAATGCC
ACTTTCAGCGCCGTGGGTGAGGCCAGCATCTGCGAGGATGACTGGAATTCCGGGAGAG
GTTCACGTGACCGTGACCCACACAGACCTGCCCTGCCACTGAAGCAGACCATCTCCC
GGCCAAGGGGTGGCCCTGCACAGGCCGATGTCTACTTGCTGCCACCAGCCCAGGGAG
CAGCTAACCTGCGGGAGTCGGCCACCATCACGTGCCTGGTGACGGCTTCTCTCCCAG
GGACGTCTCGTGAGTGGATGCAGAGGGGCAGCCCTGTCCCCGGAGAAGTATGTGA
CCAGGCCCAATGCCTGAGCCCCAGGCCGGTACTCGCCACAGCATCTG
ACCGTGTCCGAAGAGGAATGGAACACGGGGGAGACCTACACCTGCGTGGCCATGAGGC
CCTGCCAACAGGGTACCGAGAGGACCGTGGACAAGTCCACCGTAAACCCACCTGT
ACAACGTGTCCCTGGTCATGTCCGACACAGCTGGCACCTGCTACTGAGATCTGAGA
AACCGGTCTAGGTTGGAAATTGCCCCCTCCCTCCCCCCCCCTAACGTTACTGGCC
GAAGCCGCTTGAATAAGGCCGGTGTGCCCTGTCTATATGTTATTTCACCATATTG
CCGTCTTGGCAATGTGAGGGCCCGGAAACCTGCCCTGTCTTGTACGAGCATTCC
TAGGGTCTTCCCTCTGCCAACAGGAATGCAAGGTCTGTGAATGTCGTGAAGGAAG
CAGTTCTCTGGAAGCTCTGAAGACAAACAGTCTGTAGCGACCCTTGCAGGCAG
CGGAACCCCCACCTGGCGACAGGTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAG
ACCTGCAAAGCGGCACAACCCAGTGCCACGTTGTGAGTTGGATAGTTGTGAAAGAG
TCAAATGGCTCCTCAAGCGTATTCAACAAGGGCTGAAGGATGCCAGAAGGTACCC
CATTGTATGGATCTGATCTGGGCCTCGGTGCACATGCTTACATGTGTTAGTCGAG
GTTAAAAAAACGTCTAGGCCCGAACACGGGACGTGGTTCTTGTGAAACAC
GATGATAATATGGCTCCTTGTCTCTGCTCTGGTAGGCATCCTATTCCATGCCAC
CCAGGCCGACATCCAGCTGACCCAGGCCAAGCAGCCTGAGCGCCAGCGTGGTGACA
GAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGTACTCTGTAGCCTGGTACCA
CAGAACGCCAGGTAAAGGCTCCAAAGCTGCTGATCTACTGGACATCCACCCGGCACACTGG
TGTGCCAAGCAGATTCAAGCGGTAGCGGTAGCGGTACCGACTTCACCTCACCACAGCA
GCCTCCAGCCAGGGACATGCCACCTACTACTGCCAGCAATATAGCCTTATCGGT
TTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCACCTGCTT
CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTGTTGTGCGCTGCTGA
ATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCAATCG
GGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAG
TCACCCCATCAGGGCCTGAGCTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
ATCTGTTAACCTAGGCTCGAGTCAGATCGATAATCAACCTCTGGATTACAAATT
GTGAAAGATTGACTGGTATTCTTAACATGTTGCTCCTTACGCTATGTGGATAACGCT
GCTTTAATGCCTTGTATCGCTATTGCTTCCCGTATGGCTTCACTTCTCCT
GTATAAACTCTGGTTGCTGTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTG
GCGTGGTGTGCACTGTGTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCA
TGTCAGCTCCTTCCGGACTTCGCTTCCCCCTCCATTGCCACGGCGGAACCTCAT

FIGURE 22 (D)

CGCCGCCTGCCTGCCCGCTGCTGGACAGGGCTGGCTGTTGGGCACTGACAATTCCG
TGGTGGTGTGCGGGAAATCATCGCCTTCCTGGCTGCTGCCTGTGTTGCCACCTGG
ATTCTGCGCGGGACGTCCTCTGCTACGTCCTCGGCCCTCAATCCAGCGGACCTCC
TTCCCGCGCCTGCTGCCGGCTCGGCCCTTCGGCTCTCGCCTCGCCCTCAGA
CGAGTCGGATCTCCCTTGGGCCCTCCCGATCGATAAAATAAAAGATTTATTTA
GTCTCCAGAAAAAGGGGGAATGAAAGACCCCACCTGAGGTTGGCAAGCTAGCTAA
GTAACGCCATTTGCAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTCAGATC
AAGGTCAAGAACAGATGGAACAGCTGAATATGGGCCAACAGGATATCTGTGTAAGCA
GTTCCCTGCCCGGCTCAGGGCAAGAACAGATGGAACAGCTGAATATGGGCCAACAGG
ATATCTGTGGTAAGCAGTTCTGCCCGGCTCAGGGCAAGAACAGATGGTCCCCAGAT
GCGGTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCCAAGG
ACCTGAAATGACCCCTGTGCTTATTTGAACTAACCAATCAGTCGCTCTCGCTCTGT
TCGCGCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
CAGTCCTCCGATTGACTGAGTCGCCGGTACCCGTGTATCCAATAAACCCCTTGCAG
TTGCATCCGACTTGTGGTCTCGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTA
CCCGTCAGCGGGGGTCTTCATT

Figure 23(A) Gene Sequence of a Double Retrovector IgM J Chain Construct (SEQ ID NO:39).



LTR =	Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR =	Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
Blast =	Blasticidin Resistance Gene
CMV =	Simian Cytomegalovirus Promoter Region
SP =	J Chain Signal Peptide
JC =	J Chain Gene
RESE =	RNA Export and Stability Element
LTR =	Moloney Murine Leukemia Virus Long Terminal Repeat

GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCAT
 AGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGACC
 GCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAA
 TAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGGCA
 GTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAATG
 GCCCGCCTGGCATTATGCCAGTACATGACCTTATGGACTTCCACTTGGCAGTACA
 TCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATGGG
 CGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAATGG
 GAGTTGTTTGGCACCAAAATCAACGGACTTCCAAATGTCGTAACAACCTCCGCC
 CATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTCAA
 TAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTGCGTCGCCCG
 GGTACCCGTATTCCAATAAGCCTTGTCTGTTGATCCGAATCGTGGCTCGCTGT
 TCCTTGGGAGGGTCTCTGAGTGATTGACTACCCACGACGGGGTCTTCATTGGG
 GGCTCGTCCGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCACGGGAGGTA
 AGCTGGCCAGCAACTTATCTGTCTGTCGATTGTCTAGTGTCTATGTTGATGTTAT
 GCGCCTCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGACCGTGGAA
 CTGACGAGTTCTGAACACCCGGCGCAACCCCTGGGAGACGTCCCAGGGACTTGGGGC
 CGTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATA
 TGTGGTTCTGGTAGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTGG
 TTTCGGTTGGAACCGAAGCCGCGTCTGTCTGCTGCAGCGCTGCAGCATCGTCTG
 TGTTGTCTGTCTGACTGTGTTCTGTATTGTCTGAAAATTAGGGCCAGACTGTTAC
 CACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACC
 AGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGAGAATGCCAACC
 TTTAACGTCGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTTAA
 GATCAAGGTCTTTCACCTGGCCCGATGGACACCCAGACCAGGTCCCCTACATCGTGA
 CCTGGGAAGCCTGGCTTTGACCCCCCTCCCTGGGTCAAGCCCTTGTACACCCTAAG
 CCTCCGCCTCCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGAC

FIGURE 23 (B)

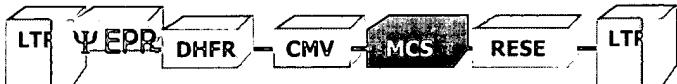
CCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCCTCGGAATTCATG
GCCAAGCCTTGTCTCAAGAAGAATCCACCCCTATTGAAAGAGCAACGGCTACAATCAA
CAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTAGCGACGGCC
GCATCTTCACTGGTGTCAATGTATATCATTTACTGGGGGACCTTGTGCAGAACTCGTG
GTGCTGGGCACTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGGATCGG
AAATGAGAACAGGGCATCTTGAGCCCCTGGACGGTGCCACAGGTGCTCTCGATC
TGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGTGATGGACAGCCACGGCAGTTGGG
ATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTGGATCCCTATG
GCTATTGCCAGGTTCAATACTATGTATTGCCCTATGCCATATAGTATTCCATATATG
GGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCCATAACCATATATGG
GGCTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGGTCTATATATGG
TCTTCCTATTGACGTATATGGCGGTCTATTGACGTATATGGCCCTCCCCATTG
ACGTCAATTACGGTAAATGGCCCGCTGGCTCAATGCCATTGACGTCAATAGGACCA
CCACCATGACGTCAATGGATGGCTCATTGCCATTCATCCGTTCTCACGCC
ATTGACGTCAATGACGGTAAATGGCCCACTTGGCAGTACATCAATACTATTAAAGTA
ACTTGGCAAGTACATTACTATTGGAAGTACGCCAGGGTACATTGGCAGTACTCCATTG
ACGTCAATGGCGGTAAATGGCCCGCGATGGCTGCCAAGTACATCCCCATTGACGTCAAT
GGGGAGGGGCAATGACGAAATGGCGTCCATTGACGTAAATGGCGGTAGGCGTGCC
TAATGGGAGGTCTATATAAGCAATGCTCGTTAGGGAACGCCATTCTGCCTGGGAGC
TCGGAGGAGCTGAAAGCTGAAAGTCAAGATGAAGAACCATTTGCTTCTGGGAGTC
CTGGCGGTTTTATTAGGCTGTCATGTGAAAGCCAAGAACAGATGAAAGGATTGTTCT
TGTTGACAACAAATGTAAGTGTGCCCGGATTACTTCCAGGATCATCCGTTCTCGAAG
ATCCTAATGAGGACATTGGAGAGAACATCCGAATTATTGTCCTCTGAACAAACAGG
GAGAACATCTGATCCCACCTCACCATTGAGAACAGAACATTGTCATGCTGA
CCTCTGAAAAAAATGTGATCCTACAGAAGTGGAGCTGGATAATCAGATAGTTACTGCTA
CCCAGAGCAATATCTGTGATGAAGACAGTGCTACAGAGACCTGCTACACTTATGACAGA
AACAAAGTGTACACAGCTGTTCCACTCGTATATGGTGGTAGAACCAAAATGGTGG
AACAGCCTAACCCCCAGATGCCGCTATCCTGACTAAGATCTGTTAACGGCCTAGGT
TTAAACTCGAGTTGACATCGATAATCAACCTCTGGATTACAAAATTGTGAAAGATTG
ACTGGTATTCTTAACTATGTTGCTCCTTACGCTATGTGGATACGCTGCTTAATGCC
TTTGTATCATGCTATTGCTCCCGTATGGCTTACATTCTCCTCTGTATAAAATCCT
GGTTGCTGTCTTTATGAGGAGTTGTGGCCCGTTGTGCAGGCAACGTGGCGTGGTGTGC
ACTGTGTTGCTGACGCAACCCCCACTGGTTGGGCATTGCCACCACTGTCAAGCTCCT
TTCCGGGACTTCGCTTCCCCCTCCATTGCCACGGCGAACATGCCGCTGCC
TTGCCGCTGACAGGGCTGGCTGGCTGTTGGCACTGACAATTCCGTGGTGTGCG
GGGAAATCATCGTCCTTCCTGGCTGCTGCCGTGTTGCCACCTGGATTCTGCGCG
GACGTCCTCTGCTACGCTCCATTGCCCGTCAATCCAGCGGACCTCCTCCCGCG
TGCTGCCGGCTTGCGGCCCTTCCCGTCTCGCCTCGCCCTCAGACGAGTCGGATC
TCCCTTGGGCCGCTCCCCGATCGATAAAATGGGAAAGATTGTTAGTCTCCAGAAA
AAGGGGGGAATGAAAGACCCCCACTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATT
TTGCAAGGCATGGAAAAATACATACTGAGAACAGGAGATCTGTGGTAAGCAGTTCTGCC
CAGATGGAACAGCTGAATATGGCCAAACAGGAGATCTGTGGTAAGCAGTTCTGCC
GGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGCCAAACAGGAGATCTGTGGT

FIGURE 23 (C)

AAGCAGTTCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
CTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGA
CCCTGTGCCTTATTGAACTAACCAATCAGTCGCTTCTGCTTCTGTCGCGCTTC
TGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCCAGTCCTCCGA
TTGACTGAGTCGCCCGGGTACCCGTATCCAATAAACCCCTTGAGTGCATTGAC
TTGTGGTCTCGCTGTTCTGGAGGGTCTCCTCTGAGTGAACCTACCGTCAGCGG
GGGTCTTCATT

FIGURE 24 (A)

Mouse dihydrofolate reductase retrovector gene construct (SEQ ID NO:40).



LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
DHFR = Mouse Dihydrofolate Reductase Gene
CMV = Simian Cytomegalovirus Promoter Region
MCS = Multiple Cloning Site (Gene Insertion Site)
RESE = RNA Export and Stability Element
LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTCAAGCCCATATATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCATAAGTAACGCC
AATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCCTGGCATTATGCCCAAGTACATGACCTTATGGGACTTCCACTTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTATGCCGTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT
GGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAATGTCGAACAACCTCCGC
CCCATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGCGCGCCAGTCTCCGATAGACTCGTCGCC
CGGGTACCGTATTCCAATAAGCCTTGTGCTGATCCGATCGTGGCTCGCT
GTTCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCACGACGGGGTCTTCAATTG
GGGGCTCGTCGGGATTGGAGACCCCTGCCAGGGACCACCGACCCACCGGGAGG
TAAGCTGGCCAGCAACTATCTGTCTGCGATTGCTAGTGTCTATGTTGATGTT
ATGCGCTCGTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCGCAACCCCTGGGAGACGTCCAGGGACTTGGGG
GCCGTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAACAGTCCCGCTCCGTCTGAATT
GCTTCGGTTGGAACCGAAGCCCGCGTCTGTGCTGCTGCAGCGCTGCAGCATCGTC
TGTGTTGCTCTGTGACTGTGTTCTGATTTGCTGAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTGTCTGCAGAATGGCCAA
CCTTTAACGTGGATGGCCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTTCACCTGGCCGATGGACACCCAGACAGGTCCCCCTACATCGT
GACCTGGGAAGCCTTGGCTTTGACCCCCCTCCGTCAAGCCCTTGTACACCCCTA

FIGURE 24 (B)

AGCCTCCGCCTCCTCTTCCATCCGCCCGTCTCTCCCCCTTGAACCTCCTCGTTCG
ACCCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTAGGCGCCGGAATTCC
GATCTGATCAAGAGACAGGGATGACCTAGGCTTGTCAAAGCTTATCCCCGCTGCCA
TCATGGTTGACCATTAATGAACTGCATCGTCCGCTGTCAGATATGGGGATTGGCAAG
AACGGAGACCTACCCCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCAAAGAATGAC
CACAAACCTCTCAGTGGAAAGTAAACAGAATCTGGTATTGGTAGGAAAACCTGGT
TCTCCATTCTGAGAAGAATCGACCTTAAAGGACAGAATTAATATAGTCTCAGTAGA
GAACCTCAAAGAACCAACGAGGAGCTCATTCTGCCAAAGTTGGATGATGCCCT
AAGACTTATTGAACAAACCGAATTGGCAAGTAAAGTAGACATGGTTGGATAGTCGGAG
GCAGTTCTGTTTACCAAGGAAGCCATGAATCAACCAGGCCACCTCAGACTCTTGTGACA
AGGATCATGCAGGAATTGAAAGTGACACGTTTCCCAGAAATTGATTTGGGGAAATA
TAAACTCTCCCAGAATACCCAGCGTCCCTCTGAGGTCCAGGAGGAAAAGGCATCA
AGTATAAGTTGAAGTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCTCT
GCTCCCTCCTAAAGCTATGCATTTCATAAGACCATGGGACTTTGCTGGCTTAGAT
CCCTATGGCTATTGCCAGGTTCAATACTATGTATTGCCATATGCTATTCC
ATATATGGGTTTCCTATTGACGTAGATAGCCCCTCCAATGGCGGTCCATATACCA
TATATGGGCTTCCTAATACGCCATAGCCACTCCCCATTGACGTCAATGGTCTCTA
TATATGGTCTTCCTATTGACGTATGGCGGTCTATTGACGTATATGGCGCTC
CCCATTGACGTCAATTACGGTAATGGCCCGCCTGGCTCAATGCCATTGACGTCAATA
GGACCACCCACCATTGACGTCAATGGGATGGCTATTGCCATTCATATCGTTCTCAC
GCCCTATTGACGTCAATGACGGTAATGGCCCATTGGCAGTACATCAATATCTATT
AATAGTAACGGCAAGTACATTACTATTGAAAGTACGCCAGGGTACATTGGCAGTACT
CCCATTGACGTCAATGGCGGTAAATGGCCCGCAGTGGCTGCAAGTACATCCCCATTGA
CGTCAATGGGAGGGCAATGACGCAAATGGCGTCCATTGACGTAAATGGCGGTAG
GCGTGCCTAATGGAGGTCTATATAAGCAATGCTCGTTAGGGACCGCATTGCCT
GGGACGTCGGAGGAGCTGAAAGCTCTAGACAATTGACGCGTAGGCCTGCGGCCGCG
TCGACCAAGGGCCAGATCTGTTAACGGCCTAGGTTAACTCGAGTTGACATCGA
TAATCAACCTCTGGATTACAAAATTGTGAAAGATTGACTGGTATTCTTAACATGTTG
CTCCTTTACGCTATGTGGATACGCTGCTTAAATGCCATTGTATCATGCTATTGCTTCC
CGTATGGCTTCATTCTCCTCTGTATAAATCCTGGTGTCTCTTATGAGGA
GTTGGCCCGTTGTCAGGCAACGTGGCGTGTGCACTGTGTTGCTGACGCAACCC
CCACTGGTTGGGCATTGCCACACCTGTCAAGCTCTTCCGGACTTCGCTTCCCC
CTCCCTATTGCCACGGCGGAACTCATGCCGCTGCCATTGCCGCTGCGACAGGGC
TCGGCTGTTGGCACTGACAATTCCGTGGTGTGCGGGAAATCATCGTCTTCC
GGCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTCTGCTACGTC
TCGGCCCTCAATCCAGCGGACCTCCTCCGCCGCTGCTGCCGCTGCGCCCT
TCCGCGTCTCGCCTCGCCCTCAGACGAGTCGGATCTCCATTGGCCCTCCCCGC
ATCGATAAAATAAAAGATTCTAGTCTCCAGAAAAAGGGGGAAATGAAAGACCCCA
CCTGTAGGTTGGCAAGCTAGCTTAAGTAACGCCATTGCAAGGCATGGAAAAATACA
TAACTGAGAATAGAGAAGTTCAGATCAAGGTCAAGGAAACAGATGAAACAGCTGAATATGG
GCCAAACAGGATATCTGTTGTAAGCAGTTCTGCCCGCAGGGCCAAGAACAGATG
GAACAGCTGAATATGGGCCAACAGGATATCTGTTGTAAGCAGTTCTGCCCGC
GGGCCAACAGATGGTCCCCAGATGCCGCTCAGCAGTTCTAGAGAACCA

FIGURE 24 (C)

TCAGATGTTCCAGGGTGCCCAAGGACCTGAAATGACCCTGTGCCTTATTGAECTAA
CCAATCAGTCGCTTCTCGCTTCTGTCGCGCTTCTGCTCCCCGAGCTCAATAAAAG
AGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACC
CGTGTATCCAATAAACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTGG
GAGGGTCTCCTCTGAGTGATTGACTACCCGTCAAGCGGGGTCTTCATT 4354

1 - 763	HCMV-MOMUSV CHIMERIC 5'LTR
833 - 1642	EXTENDED PACKAGING REGION
1712 - 2272	MOUSE DHFR GENE CODING REGION
2355 - 3038	SIMIAN CMV PROMOTER
3029 - 3114	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3121 - 3721	RESE
3761 - 4354	3'LTR

Figure 25(A)

Glutamine synthase Retrovector gene construct (SEQ ID NO:41)



LTR = Human CMV/Moloney Murine Sarcoma Virus Long Terminal Repeat Fusion
Ψ EPR = Moloney Murine Leukemia Virus Psi Region and Extended Viral Packaging Region
DHFR = Mouse Glutamine Synthase Gene
CMV = Simian Cytomegalovirus Promoter Region
MCS = Multiple Cloning Site (Gene Insertion Site)
RESE = RNA Export and Stability Element
LTR = Moloney Murine Leukemia Virus Long Terminal Repeat

1 GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCAATTAGTTCA
ATAGCCCATAATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCTGGCTGA
CCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTCCCAGTAGAACGCC
AATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTTGG
CAGTACATCAAGTGTATCATATGCCAAGTACGCCCTATTGACGTCAATGACGGTAAA
TGGCCCGCTGGCATTATGCCCAAGTACATGACCTTATGGGACTTTCTACTGGCAGTA
CATCTACGTATTAGTCATCGCTATTACCATGGTATGCGGTTTGGCAGTACATCAATG
GGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT
GGGAGTTGTTGGCACCAAAATCAACGGGACTTCCAAATGTCGAACAACACTCCGC
CCCATTGACGCAAATGGCGGTAGGCATGTACGGTGGGAGGTCTATATAAGCAGAGCTC
AATAAAAGAGCCCACAACCCCTCACTCGGCGGCCAGTCTCCGATAGACTGCGTCGCC
CGGGTACCGTATTCCAATAAGCCTTGTGCTTGCATCCGAATCGTGGCTCGCT
GTTCCCTGGGAGGGTCTCCTCTGAGTGAATTGACTACCCACGACGGGGTCTTCATTG
GGGGCTCGTCCGGATTGGAGACCCCTGCCAGGGACCACGACCCACCACGGGAGG
TAAGCTGGCAGCAACTATCTGTCTGTCGATTGCTAGTGTCTATGTTGATGTT
ATGCGCCTCGTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGG
AACTGACGAGTTCTGAACACCCGGCGAACCCCTGGGAGACGTCCAGGGACTTGGGG
GCCGTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCGTCAAGGA
TATGTGGTTCTGGTAGGAGACGAGAACCTAAACAGTCCCGCTCCGTCTGAATT
GCTTTCGGTTGGAACCGAAGCCCGCGTCTGTCTGCTGCAGCGCTGCAGCATCGTC
TGTGTTGTCTGTCTGACTGTGTTCTGTATTGCTGAAATTAGGGCCAGACTGTT
ACCACTCCCTTAAGTTGACCTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAA
CCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAAGATGGCCAA
CCTTTAACGTGGATGGCCGAGACGGCACCTTAACCGAGACCTCATCACCCAGGTT
AAGATCAAGGTCTTACCTGGCCCGCATGGACACCCAGACCGAGGTCCCCTACATCGT

FIGURE 25 (B)

GACCTGGGAAGCCTTGGCTTGTACACCCCTACCCCTGGGTCAAGCCCTTGTACACCC
AGCCTCCGCCTCCTCTTCCATCCGCCCGTCTCTCCCTGAACCTCCTCGTT
ACCCCGCCTCGATCCTCCCTTATCCAGCCCTCACTCCTCTCTAGGCGCCGAAATTCC
GATCTGATCAAGAGACAGGATGAACCAGGCCACCTCAGCAAGTTCCACTTGAACAAA
GGCATCAAGCAAATGTACATGTCCCTGCCAGGGTGAGAAAGTCCAAGCCATGTATAT
CTGGGTGATGGTACCGAGAAGGACTGCGCTGCAAGACCCGTACCTGGACTGTGAGC
CCAAGTGTGGAAGAGTTACCTGAGTGGAACTTGATGGCTCTAGTACCTTCAGTCT
GAAGGCTCCAACAGCGACATGTACCTCCATCCTGTTGCCATGTTGAGACCCCTCCG
CAAAGACCCACAAGCTGGTGTATGTGAAGTTCAAGTATAACCGGAAGCCTGCAG
AGACCAACTTGAGGCACATCTGTAACGGATAATGGACATGGTGAGCAACCAGCACCC
TGGTTGGAATGGAGCAGGAATATACTCTTATGGGAACAGACGGCCACCCATTGGTT
GCCTTCCAATGGCTTCCCTGGACCCCAAGGCCGTATTACTGCGGTGTGGAGCAGACA
AGGCCTACGGCAGGGACATCGTGGAGGCTCACTACCGGGCTGCTGTATGCTGGAGTC
AAGATCACGGGACAAATGCGGAGGTTATGCCTGCCAGTGGAAATTCCAGATAGGACC
CTGTGAGGGGATCCGAATGGGAGATCATCTTGGATAGCCGTTTATCTGCATCGG
TGTGCGAAGACTTGGGTGATAGCAACCTTGACCCCAAGCCCATTCCAGGGAACTGG
AATGGTGCAGGCTGCCATACCAACTTCAGCACCAAGGCCATGCGGGAGGAGATGGTCT
GAAGTGCATTGAGGAGGCCATTGACAAACTGAGCAAGAGGCCAGTACACATCCGCG
CCTACGATCCAAGGGGGCCTGGACAACGCCGGCGTCTGACTGGATTCCACGAAACC
TCCAACATCAACGACTTTCTGCCGGTGTGCCAACGCCGGTGCAGTATCCGATTCC
CCGGACTGTGCCAGGAGAAGAAGGGCTACTTGAGACCGTGGCCATTGCCATT
GTGACCCCTATGCCGGTACAGAACGCCATCGTCCGACGTCTCCTCAACGAAACAGGC
GACGAACCTTCAATACAAGAACTAAGGATCCCTATGGCTATTGGCCAGGTTCAATAC
TATGTATTGGCCCTATGCCATATAGTATTCCATATATGGGTTTCATTGACGTAGAT
AGCCCTCCAATGGCGGTCCATATACCATATATGGGCTTCATAACGCCATA
GCCACTCCCCATTGACGTCAATGGTCTCTATATGGTCTTCCTATTGACGTCAATT
GGCGGTCTATTGACGTATGGCGCTCCCCATTGACGTCAATTACGGTAAATGGC
CCGCCTGGCTCAATGCCATTGACGTCAATAGGACCAACCCACATTGACGTCAATGGG
TGGCTATTGCCATTCATATCCGTTCTCACGCCCTATTGACGTCAATGACGGTAAA
TGGCCACTTGGCAGTACATCAATATCTATTAAATAGTAACGGCAAGTACATTACTAT
TGGAAAGTACGCCAGGGTACATTGGCAGTACTCCCATTGACGTCAATGGCGTAAATGGC
CCGCGATGGCTCCAAGTACATCCCATTGACGTCAATGGGAGGGCAATGACGCAA
TGGCGTCCATTGACGTAAATGGCGGTAGGCGTGCCTAATGGGAGGTCTATATAAGC
AATGCTCGTTAGGAACGCCATTCTGCCTGGGACGTGGAGGAGCTGAAAGCTTC
TAGACAATTGACCGTAGGCCTGCCCGCGTCGACCAAGGCCAGATCTGTTAACCG
GTCCTAGGTTAAACTCGAGTTGACATCGATAATCAACCTCTGGATTACAAAATTGT
GAAAGATTGACTGGTATTCTTAACATATGTGCTCCTTTACGCTATGTGGATACGCTGC
TTAATGCCCTTGTATCATGCTATTGCTTCCGTATGGCTTTCATTTCCTCCTTGT
ATAAAATCCTGGTTGCTGCTCTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGC
GTGGTGTGCACTGTGTTGCTGACGCAACCCCACTGGTTGGGCAATTGCCACCCACTG
TCAGCTCCTTCCGGACTTCGCTTCCCTCCATTGCCACGGCGGAACTCATCG
CCGCCTGCCATTGCCCGCTGGACAGGGGCTGGCTGTTGGGACTGACAATTCCGTG
GTGTTGTCGGGAAATCATCGTCCTTCCATTGGCTGCTGCCCTGTGTTGCCACCTGGAT

FIGURE 25 (C)

TCTGCGCGGGACGTCCTCTGCTACGTCCCTCGGCCCTCAATCCAGCGGACCTCCTT
CCCGCGGCCTGCTGCCGGCTCTGCCGCTCTCCGCGTCTCGCCTCGCCCTCAGACG
AGTCGGATCTCCCTTGGGCCCTCCCGCATCGATAAAATAAAAGATTTATTTAGT
CTCCAGAAAAAGGGGGAAATGAAAGACCCCACCTGAGTTGGCAAGCTAGCTTAAGT
AACGCCATTTGCAAGGCATGGAAAATACATAACTGAGAATAGAGAAGTCAGATCAA
GGTCAGGAACAGATGGAACAGCTGAATATGGGCCAACAGGATATCTGTGGTAAGCAGT
TCCTGCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAACAGGAT
ATCTGTGGTAAGCAGTTCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGC
GGTCCAGCCCTCAGCAGTTCTAGAGAACCATCAGATGTTCCAGGGTGCCCAAGGAC
CTGAAATGACCTGTGCCTATTGAACTAACCAATCAGTCGCTCTCGCTCTGTT
GCGCGCTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTGGGGCGCCA
GTCCTCGATTGACTGAGTCGCCGGTACCCGTATCCAATAAACCCCTCTGCAGTT
GCATCCGACTTGTGGTCTGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACC
CGTCAGCGGGGTCTTCATT 4797

1 - 763	HCMV-MOMUSV CHIMERIC 5'LTR
833 - 1642	EXTENDED PACKAGING REGION
1677 - 2795	MOUSE GLUTAMINE SYNTHASE GENE CODING REGION
2805 - 3472	SIMIAN CMV PROMOTER
3473 - 3558	MULTIPLE CLONING SITE (SITE OF GENE INSERTION)
3565 - 4165	RESE
4205 - 4797	3'LTR